

11-88L.ST25.txt
SEQUENCE LISTING

<110> Seed, Brian
Aruffo, Alejandro
Camerini, David

<120> CD27 Coding Sequence

<130> 11-88L

<140> US 09/836,544
<141> 2001-04-17

<150> US 07/983,647
<151> 1992-12-01

<150> US 07/553,759
<151> 1990-07-13

<150> US 07/498,809
<151> 1990-03-23

<150> US 07/379,076
<151> 1989-07-13

<150> US 07/160,416
<151> 1988-02-25

<160> 41

<170> PatentIn version 3.3

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<212> DNA
<213> artificial

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<223> Nucleotide sequence of piH3 vector

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atactgtcct tctagtgttag ccgtagtttag gccaccactt caagaactct gtagcaccgc 180
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gctcgtcagg ggggcggagc ctatggaaaa acgccagcaa cgccgaatta cccgcgggtgtt 600
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<222> (7)..(1059)

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Phe Asn Val Ser Ser Lys Gly Ala Val Ser Lys Glu Ile Thr Asn Ala	
15 20 25 30	
ttg gaa acc tgg ggt gcc ttg ggt cag gac atc aac ttg gac att cct	144
Leu Glu Thr Trp Gly Ala Leu Gly Gln Asp Ile Asn Leu Asp Ile Pro	
35 40 45	
agt ttt caa atg agt gat gat att gac gat ata aaa tgg gaa aaa act	192
Ser Phe Gln Met Ser Asp Asp Ile Asp Asp Ile Lys Trp Glu Lys Thr	
50 55 60	
tca gac aag aaa aag att gca caa ttc aga aaa gag aaa gag act ttc	240
Ser Asp Lys Lys Lys Ile Ala Gln Phe Arg Lys Glu Lys Glu Thr Phe	
65 70 75	
aag gaa aaa gat aca tat aag cta ttt aaa aat gga act ctg aaa att	288
Lys Glu Lys Asp Thr Tyr Lys Leu Phe Lys Asn Gly Thr Leu Lys Ile	
80 85 90	
aag cat ctg aag acc gat gat cag gat atc tac aag gta tca ata tat	336
Lys His Leu Lys Thr Asp Asp Gln Asp Ile Tyr Lys Val Ser Ile Tyr	
95 100 105 110	
gat aca aaa gga aaa aat gtg ttg gaa aaa ata ttt gat ttg aag att	384
Asp Thr Lys Gly Lys Asn Val Leu Glu Lys Ile Phe Asp Leu Lys Ile	
115 120 125	
caa gag agg gtc tca aaa cca aag atc tcc tgg act tgt atc aac aca	432
Gln Glu Arg Val Ser Lys Pro Lys Ile Ser Trp Thr Cys Ile Asn Thr	
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acc ctg acc tgt gag gta atg aat gga act gac ccc gaa tta aac ctg	480
Thr Leu Thr Cys Glu Val Met Asn Gly Thr Asp Pro Glu Leu Asn Leu	

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aaa gtc agc aag gaa tcc agt gtc gag cct gtc agc tgt cca gag aaa Lys Val Ser Lys Glu Ser Ser Val Glu Pro Val Ser Cys Pro Glu Lys 195 200 205			624
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ttg atg gtc ttt gtg gca ctg ctc gtt ttc tat atc acc aaa agg aaa Leu Met Val Phe Val Ala Leu Leu Val Phe Tyr Ile Thr Lys Arg Lys 225 230 235			720
aaa cag agg agt cg ^g aga aat gat gag gag ctg gag aca aga gcc cac Lys Gln Arg Ser Arg Arg Asn Asp Glu Glu Leu Glu Thr Arg Ala His 240 245 250			768
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gg ^t cat cgt tcc cag gca cct agt cat cgt ccc cc ^g cct cct gga cac Gly His Arg Ser Gln Ala Pro Ser His Arg Pro Pro Pro Pro Gly His 290 295 300			912
cgt gtt cag cac cag cct cag aag agg cct cct gct cc ^g tcg ggc aca Arg Val Gln His Gln Pro Gln Lys Arg Pro Pro Ala Pro Ser Gly Thr 305 310 315			960
caa gtt cac cag cag aaa ggc cc ^g ccc ctc ccc aga cct cga gtt cag Gln Val His Gln Gln Lys Gly Pro Pro Leu Pro Arg Pro Arg Val Gln 320 325 330			1008
cca aaa cct ccc cat ggg gca gca gaa aac tca ttg tcc cct tcc tct Pro Lys Pro Pro His Gly Ala Ala Glu Asn Ser Leu Ser Pro Ser Ser 335 340 345 350			1056
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<212> PRT
<213> Homo sapiens

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35 40 45

Gln Met Ser Asp Asp Ile Asp Asp Ile Lys Trp Glu Lys Thr Ser Asp
50 55 60

Lys Lys Lys Ile Ala Gln Phe Arg Lys Glu Lys Glu Thr Phe Lys Glu
65 70 75 80

Lys Asp Thr Tyr Lys Leu Phe Lys Asn Gly Thr Leu Lys Ile Lys His
85 90 95

Leu Lys Thr Asp Asp Gln Asp Ile Tyr Lys Val Ser Ile Tyr Asp Thr
100 105 110

Lys Gly Lys Asn Val Leu Glu Lys Ile Phe Asp Leu Lys Ile Gln Glu
115 120 125

Arg Val Ser Lys Pro Lys Ile Ser Trp Thr Cys Ile Asn Thr Thr Leu
130 135 140

Thr Cys Glu Val Met Asn Gly Thr Asp Pro Glu Leu Asn Leu Tyr Gln
145 150 155 160

Asp Gly Lys His Leu Lys Leu Ser Gln Arg Val Ile Thr His Lys Trp
165 170 175

Thr Thr Ser Leu Ser Ala Lys Phe Lys Cys Thr Ala Gly Asn Lys Val
180 185 190

Ser Lys Glu Ser Ser Val Glu Pro Val Ser Cys Pro Glu Lys Gly Leu
195 200 205

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Asp Ile Tyr Leu Ile Ile Gly Ile Cys Gly Gly Ser Leu Leu Met
210 215 220

Val Phe Val Ala Leu Leu Val Phe Tyr Ile Thr Lys Arg Lys Lys Gln
225 230 235 240

Arg Ser Arg Arg Asn Asp Glu Glu Leu Glu Thr Arg Ala His Arg Val
245 250 255

Ala Thr Glu Glu Arg Gly Arg Lys Pro His Gln Ile Pro Ala Ser Thr
260 265 270

Pro Gln Asn Pro Ala Thr Ser Gln His Pro Pro Pro Pro Pro Gly His
275 280 285

Arg Ser Gln Ala Pro Ser His Arg Pro Pro Pro Pro Gly His Arg Val
290 295 300

Gln His Gln Pro Gln Lys Arg Pro Pro Ala Pro Ser Gly Thr Gln Val
305 310 315 320

His Gln Gln Lys Gly Pro Pro Leu Pro Arg Pro Arg Val Gln Pro Lys
325 330 335

Pro Pro His Gly Ala Ala Glu Asn Ser Leu Ser Pro Ser Ser Asn
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<222> (13)..(723)

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Leu Ser Val Val Cys Leu Leu His Cys Phe Gly Phe Ile Ser Cys Phe
15 20 25

tcc caa caa ata tat ggt gtt gtg tat ggg aat gta act ttc cat gta 147
Ser Gln Gln Ile Tyr Gly Val Val Tyr Gly Asn Val Thr Phe His Val
30 35 40 45

cca agc aat gtg cct tta aaa gag gtc cta tgg aaa aaa caa aag gat 195
Pro Ser Asn Val Pro Leu Lys Glu Val Leu Trp Lys Lys Gln Lys Asp

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aac tta aca tca tca gat gaa gat gag tat gaa atg gaa tcg cca aat Asn Leu Thr Ser Ser Asp Glu Asp Glu Tyr Glu Met Glu Ser Pro Asn 95 100 105	339
att act gat acc atg aag ttc ttt ctt tat gtg ctt gag tct ctt cca Ile Thr Asp Thr Met Lys Phe Phe Leu Tyr Val Leu Glu Ser Leu Pro 110 115 120 125	387
tct ccc aca cta act tgt gca ttg act aat gga agc att gaa gtc caa Ser Pro Thr Leu Thr Cys Ala Leu Thr Asn Gly Ser Ile Glu Val Gln 130 135 140	435
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agc aat cca tta ttt aat aca aca tca tca atc att ttg aca acc tgt Ser Asn Pro Leu Phe Asn Thr Thr Ser Ser Ile Ile Leu Thr Thr Cys 190 195 200 205	627
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<213> Homo sapiens

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Ile Tyr Gly Val Val Tyr Gly Asn Val Thr Phe His Val Pro Ser Asn
35 40 45

Val Pro Leu Lys Glu Val Leu Trp Lys Lys Gln Lys Asp Lys Val Ala
50 55 60

Glu Leu Glu Asn Ser Glu Phe Arg Ala Phe Ser Ser Phe Lys Asn Arg
65 70 75 80

Val Tyr Leu Asp Thr Val Ser Gly Ser Leu Thr Ile Tyr Asn Leu Thr
85 90 95

Ser Ser Asp Glu Asp Glu Tyr Glu Met Glu Ser Pro Asn Ile Thr Asp
100 105 110

Thr Met Lys Phe Phe Leu Tyr Val Leu Glu Ser Leu Pro Ser Pro Thr
115 120 125

Leu Thr Cys Ala Leu Thr Asn Gly Ser Ile Glu Val Gln Cys Met Ile
130 135 140

Pro Glu His Tyr Asn Ser His Arg Gly Leu Ile Met Tyr Ser Trp Asp
145 150 155 160

Cys Pro Met Glu Gln Cys Lys Arg Asn Ser Thr Ser Ile Tyr Phe Lys
165 170 175

Met Glu Asn Asp Leu Pro Gln Lys Ile Gln Cys Thr Leu Ser Asn Pro
180 185 190

Leu Phe Asn Thr Thr Ser Ser Ile Ile Leu Thr Thr Cys Ile Pro Ser
195 200 205

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210 215 220

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<223> Nucleotide sequence of the piH3M vector.

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atgtctggat cctgtggaat gtgtgtcagt tagggtgtgg aaagtccccca ggctccccag	3600
caggcagaag tatgcaaagc atgcatctca attagtcagc aaccagggtgt ggaaagtccc	3660
caggctcccc agcaggcaga agtatgcaaa gcatgcattt caattagtca gcaaccatag	3720

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tccccccctt	aactccgccc	atcccgcccc	taactccgcc	cagttccgcc	cattctccgc	3780
cccatggctg	actaattttt	tttatttatg	cagaggccga	ggccgcctcg	gcctctgagc	3840
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<211> 1514
<212> DNA
<213> Homo sapiens

<220>
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					Met Leu Arg Leu Leu		
					1 5		
	ttg gct ctc aac tta ttc cct tca att caa gta aca gga aac aag att						162
	Leu Ala Leu Asn Leu Phe Pro Ser Ile Gln Val Thr Gly Asn Lys Ile						
	10 15 20						
	ttg gtg aag cag tcg ccc atg ctt gta gcg tac gac aat gcg gtc aac						210
	Leu Val Lys Gln Ser Pro Met Leu Val Ala Tyr Asp Asn Ala Val Asn						
	25 30 35						
	ctt agc tgc aag tat tcc tac aat ctc ttc tca agg gag ttc cgg gca						258
	Leu Ser Cys Lys Tyr Ser Tyr Asn Leu Phe Ser Arg Glu Phe Arg Ala						
	40 45 50						
	tcc ctt cac aaa gga ctg gat agt gct gtg gaa gtc tgt gtt gta tat						306
	Ser Leu His Lys Gly Leu Asp Ser Ala Val Glu Val Cys Val Val Tyr						
	55 60 65						
	ggg aat tac tcc cag cag ctt cag gtt tac tca aaa acg ggg ttc aac						354
	Gly Asn Tyr Ser Gln Gln Leu Gln Val Tyr Ser Lys Thr Gly Phe Asn						
	70 75 80 85						
	tgt gat ggg aaa ttg ggc aat gaa tca gtg aca ttc tac ctc cag aat						402
	Cys Asp Gly Lys Leu Gly Asn Glu Ser Val Thr Phe Tyr Leu Gln Asn						
	90 95 100						
	ttg tat gtt aac caa aca gat att tac ttc tgc aaa att gaa gtt atg						450
	Leu Tyr Val Asn Gln Thr Asp Ile Tyr Phe Cys Lys Ile Glu Val Met						
	105 110 115						
	tat cct cct tac cta gac aat gag aag agc aat gga acc att atc						498
	Tyr Pro Pro Tyr Leu Asp Asn Glu Lys Ser Asn Gly Thr Ile Ile						
	120 125 130						
	cat gtg aaa ggg aaa cac ctt tgt cca agt ccc cta ttt ccc gga cct						546
	His Val Lys Gly Lys His Leu Cys Pro Ser Pro Leu Phe Pro Gly Pro						
	135 140 145						
	tct aag ccc ttt tgg gtg ctg gtg gtt ggt gga gtc ctg gct tgc						594
	Ser Lys Pro Phe Trp Val Leu Val Val Gly Gly Val Leu Ala Cys						

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tat agc ttg cta gta aca gtg gcc ttt att att ttc tgg gtg agg agt Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser 170	175		180	642
aag agg agc agg ctc ctg cac agt gac tac atg aac atg act ccc cgc Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg 185	190		195	690
cgc ccc ggg ccc acc cgc aag cat tac cag ccc tat gcc cca cca cgc Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg 200	205		210	738
gac ttc gca gcc tat cgc tcc tgacacggac gcctatccag aagccagccg Asp Phe Ala Ala Tyr Arg Ser 215	220			789
gctggcagcc cccatctgct caatatcaact gctctggata ggaaatgacc gccatctcca gccggccacc tcagccccctg ttgggccacc aatgccaatt tttctcgagt gactagacca aatatcaaga tcattttgag actctgaaat gaagtaaaag agatttcctg tgacaggcca agtcttacag tgccatggcc cacattccaa cttaccatgt acttagtgac ttgactgaga agtttaggta gaaaacaaaaa agggagtgga ttctggagc ctctccctt tctcactcac ctgcacatct cagtcaagca aagtgtggta tccacagaca ttttagttgc agaagaaagg cttagaaatc attccctttg gttaaatggg tggtaatct tttggtagt gggtaaacg gggtaagtta gagtaggggg agggatagga agacatattt aaaaaccatt aaaacactgt ctcccactca tgaaatgagc cacgtatc ctatataatg ctgtttccct ttagtttaga aatacataga cattgtctt tatgaattct gatcatattt agtcattttg accaaatgag ggatttggtc aaatgagggta ttccctcaaa gcaatatcag gtaaaccagg ttgctttccct cactccctgt catgagactt cagtgttaat gttcacaata tactttcgaa agaataaaat agttc				1514

<210> 8
<211> 220
<212> PRT
<213> Homo sapiens

<400> 8

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1 5 10 15

Thr Gly Asn Lys Ile Leu Val Lys Gln Ser Pro Met Leu Val Ala Tyr
20 25 30

Asp Asn Ala Val Asn Leu Ser Cys Lys Tyr Ser Tyr Asn Leu Phe Ser
35 40 45

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Arg Glu Phe Arg Ala Ser Leu His Lys Gly Leu Asp Ser Ala Val Glu
 50 55 60

Val Cys Val Val Tyr Gly Asn Tyr Ser Gln Gln Leu Gln Val Tyr Ser
 65 70 75 80

Lys Thr Gly Phe Asn Cys Asp Gly Lys Leu Gly Asn Glu Ser Val Thr
 85 90 95

Phe Tyr Leu Gln Asn Leu Tyr Val Asn Gln Thr Asp Ile Tyr Phe Cys
 100 105 110

Lys Ile Glu Val Met Tyr Pro Pro Tyr Leu Asp Asn Glu Lys Ser
 115 120 125

Asn Gly Thr Ile Ile His Val Lys Gly Lys His Leu Cys Pro Ser Pro
 130 135 140

Leu Phe Pro Gly Pro Ser Lys Pro Phe Trp Val Leu Val Val Val Gly
 145 150 155 160

Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile
 165 170 175

Phe Trp Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met
 180 185 190

Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro
 195 200 205

Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser
 210 215 220

<210> 9
 <211> 1665
 <212> DNA
 <213> Homo sapiens

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 gggtggggtg ctgagcggcc tccagtgtct gaggactcat ttaagagaag gaaaaagggt 300
 ggaccgggtg gggagtggcc gggctgtcc aggcaaggcc gctgcttgg gaggaagaag 360

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ggaggtcaat	gtctacggct	ccggcaccct	ggtcctggtg	acagaggaac	agtcccaagg	900
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<210> 10
<211> 2290
<212> DNA
<213> Homo sapiens

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	ttgagccccc	gtggatcaac	gtgctccagg	aggactctgt	gactctgaca	tgccaggggg	180
	ctcgcagccc	tgagagcgcac	tccattcagt	ggttccacaa	tggaatctc	attcccaccc	240
	acacgcagcc	cagctacagg	ttcaaggcca	acaacaatga	cagcggggag	tacacgtgcc	300
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11-88L.ST25.txt

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tgactcttcc tcccaacgac catgtcaaca gtaataacta aagagtaacg ttatgccatg	960
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taactttgct taaactacaa acacaagcaa aacttcacgg ggtcatacta catacaagca	1140
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cagccaatca caagcagcct actaacatat aattaggtga cttagggactt tctaagaaga	1260
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taagcgattc tcatgcctca gcctcccagt agctggattt agaggcatgt gccatcatac	1560
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aggactcttc cagagtcatc tacctgagtc ccaaagctcc ctgtcctgaa agccacagac	2040
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gacttcagaa atgttaaaat agactaacct ctaacaacaa attaaaagtg attgtttcaa	2280

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ggtgaaaaaa 2290

<210> 11
<211> 1474
<212> DNA
<213> *Homo sapiens*

<220>
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 <222> (94)..(984)

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				Met	Thr	Thr	Pro	Arg	Asn	Ser						
				1				5								
gta	aat	ggg	act	ttc	ccg	gca	gag	cca	atg	aaa	ggc	cct	att	gct	atg	162
Val	Asn	Gly	Thr	Phe	Pro	Ala	Glu	Pro	Met	Lys	Gly	Pro	Ile	Ala	Met	
10				15					20							
caa	tct	ggt	cca	aaa	cca	ctc	ttc	agg	agg	atg	tct	tca	ctg	gtg	ggc	210
Gln	Ser	Gly	Pro	Lys	Pro	Leu	Phe	Arg	Arg	Met	Ser	Ser	Leu	Val	Gly	
25				30					35							
ccc	acg	caa	agc	ttc	ttc	atg	agg	gaa	tct	aag	act	ttg	ggg	gct	gtc	258
Pro	Thr	Gln	Ser	Phe	Phe	Met	Arg	Glu	Ser	Lys	Thr	Leu	Gly	Ala	Val	
40				45					50				55			
cag	att	atg	aat	ggg	ctc	ttc	cac	att	gcc	ctg	ggg	ggt	ctt	ctg	atg	306
Gln	Ile	Met	Asn	Gly	Leu	Phe	His	Ile	Ala	Leu	Gly	Gly	Leu	Leu	Met	
60				65					70							
atc	cca	gca	ggg	atc	tat	gca	ccc	atc	tgt	gtg	act	gtg	tgg	tac	cct	354
Ile	Pro	Ala	Gly	Ile	Tyr	Ala	Pro	Ile	Cys	Val	Thr	Val	Trp	Tyr	Pro	
75				80					85							
ctc	tgg	gga	ggc	att	atg	tat	att	att	tcc	gga	tca	ctc	ctg	gca	gca	402
Leu	Trp	Gly	Gly	Ile	Met	Tyr	Ile	Ile	Ser	Gly	Ser	Leu	Leu	Ala	Ala	
90				95					100							
acg	gag	aaa	aac	tcc	agg	aag	tgt	ttg	gtc	aaa	gga	aaa	atg	ata	atg	450
Thr	Glu	Lys	Asn	Ser	Arg	Lys	Cys	Leu	Val	Lys	Gly	Lys	Met	Ile	Met	
105				110					115							
aat	tca	ttg	agc	ctc	ttt	gct	gcc	att	tct	gga	atg	att	ctt	tca	atc	498
Asn	Ser	Leu	Ser	Leu	Phe	Ala	Ala	Ile	Ser	Gly	Met	Ile	Leu	Ser	Ile	
120				125					130				135			
atg	gac	ata	ctt	aat	att	aaa	att	tcc	cat	ttt	tta	aaa	atg	gag	agt	546
Met	Asp	Ile	Leu	Asn	Ile	Lys	Ile	Ser	His	Phe	Leu	Lys	Met	Glu	Ser	
140				145					150							
ctg	aat	ttt	att	aga	gct	cac	aca	cca	tat	att	aac	ata	tac	aac	tgt	594
Leu	Asn	Phe	Ile	Arg	Ala	His	Thr	Pro	Tyr	Ile	Asn	Ile	Tyr	Asn	Cys	
155				160					165							
gaa	cca	gct	aat	ccc	tct	gag	aaa	aac	tcc	cca	tct	acc	caa	tac	tgt	642
Glu	Pro	Ala	Asn	Pro	Ser	Glu	Lys	Asn	Ser	Pro	Ser	Thr	Gln	Tyr	Cys	

11-88L.ST25.txt

170	175	180	
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ttt gcc ttc ttc cag gaa ctt gta ata gct ggc atc gtt gag aat gaa Phe Ala Phe Phe Gln Glu Leu Val Ile Ala Gly Ile Val Glu Asn Glu	200 205	210 215	738
tgg aaa aga acg tgc tcc aga ccc aaa tct aac ata gtt ctc ctg tca Trp Lys Arg Thr Cys Ser Arg Pro Lys Ser Asn Ile Val Leu Leu Ser	220	225	786
gca gaa gaa aaa aaa gaa cag act att gaa ata aaa gaa gaa gtg gtt Ala Glu Glu Lys Lys Glu Gln Thr Ile Glu Ile Lys Glu Glu Val Val	235	240	834
ggg cta act gaa aca tct tcc caa cca aag aat gaa gaa gac att gaa Gly Leu Thr Glu Thr Ser Ser Gln Pro Lys Asn Glu Glu Asp Ile Glu	250	255	882
att att cca atc caa gaa gag gaa gaa gaa aca gag acg aac ttt Ile Ile Pro Ile Gln Glu Glu Glu Glu Thr Glu Thr Asn Phe	265 270	275	930
cca gaa cct ccc caa gat cag gaa tcc tca cca ata gaa aat gac agc Pro Glu Pro Pro Gln Asp Gln Glu Ser Ser Pro Ile Glu Asn Asp Ser	280 285	290 295	978
tct cct taagtgattt cttctgtttt ctgtttcctt ttttaaacat tagtgttcat Ser Pro			1034
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<210> 12
<211> 297
<212> PRT
<213> *Homo sapiens*

<400> 12

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20

25

30

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 35 40 45

Ser Lys Thr Leu Gly Ala Val Gln Ile Met Asn Gly Leu Phe His Ile
 50 55 60

Ala Leu Gly Gly Leu Leu Met Ile Pro Ala Gly Ile Tyr Ala Pro Ile
 65 70 75 80

Cys Val Thr Val Trp Tyr Pro Leu Trp Gly Gly Ile Met Tyr Ile Ile
 85 90 95

Ser Gly Ser Leu Leu Ala Ala Thr Glu Lys Asn Ser Arg Lys Cys Leu
 100 105 110

Val Lys Gly Lys Met Ile Met Asn Ser Leu Ser Leu Phe Ala Ala Ile
 115 120 125

Ser Gly Met Ile Leu Ser Ile Met Asp Ile Leu Asn Ile Lys Ile Ser
 130 135 140

His Phe Leu Lys Met Glu Ser Leu Asn Phe Ile Arg Ala His Thr Pro
 145 150 155 160

Tyr Ile Asn Ile Tyr Asn Cys Glu Pro Ala Asn Pro Ser Glu Lys Asn
 165 170 175

Ser Pro Ser Thr Gln Tyr Cys Tyr Ser Ile Gln Ser Leu Phe Leu Gly
 180 185 190

Ile Leu Ser Val Met Leu Ile Phe Ala Phe Phe Gln Glu Leu Val Ile
 195 200 205

Ala Gly Ile Val Glu Asn Glu Trp Lys Arg Thr Cys Ser Arg Pro Lys
 210 215 220

Ser Asn Ile Val Leu Leu Ser Ala Glu Glu Lys Lys Glu Gln Thr Ile
 225 230 235 240

Glu Ile Lys Glu Glu Val Val Gly Leu Thr Glu Thr Ser Ser Gln Pro
 245 250 255

Lys Asn Glu Glu Asp Ile Glu Ile Ile Pro Ile Gln Glu Glu Glu
 260 265 270

11-88L.ST25.txt

Glu Glu Thr Glu Thr Asn Phe Pro Glu Pro Pro Gln Asp Gln Glu Ser
275 280 285

Ser Pro Ile Glu Asn Asp Ser Ser Pro
290 295

<210> 13
<211> 1888
<212> DNA
<213> *Homo sapiens*

<220>
<221> CDS
<222> (13)..(1608)

11-88L.ST25.txt

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ctg gac ctg cgg ccc caa ggg ctg gag ctg ttt gag aac acc tcg gcc Leu Asp Leu Arg Pro Gln Gly Leu Glu Leu Phe Glu Asn Thr Ser Ala 190 195 200 205	627
ccc tac cag ctc cag acc ttt gtc ctg cca gcg act ccc cca caa ctt Pro Tyr Gln Leu Gln Thr Phe Val Leu Pro Ala Thr Pro Pro Gln Leu 210 215 220	675
gtc agc ccc cgg gtc cta gag gtg gac acg cag ggg acc gtg gtc tgc Val Ser Pro Arg Val Leu Glu Val Asp Thr Gln Gly Thr Val Val Cys 225 230 235	723
tcc ctg gac ggg ctg ttc cca gtc tcg gag gcc cag gtc cac ctg gca Ser Leu Asp Gly Leu Phe Pro Val Ser Glu Ala Gln Val His Leu Ala 240 245 250	771
ctg ggg gac cag agg ttg aac ccc aca gtc acc tat ggc aac gac tcc Leu Gly Asp Gln Arg Leu Asn Pro Thr Val Thr Tyr Gly Asn Asp Ser 255 260 265	819
tcc tcg gcc aag gcc tca gtc agt gtg acc gca gag gac gag ggc acc Phe Ser Ala Lys Ala Ser Val Ser Val Thr Ala Glu Asp Glu Gly Thr 270 275 280 285	867
cag cgg ctg acg tgt gca gta ata ctg ggg aac cag agc cag gag aca Gln Arg Leu Thr Cys Ala Val Ile Leu Gly Asn Gln Ser Gln Glu Thr 290 295 300	915
ctg cag aca gtg acc atc tac agc ttt ccg gcg ccc aac gtg att ctg Leu Gln Thr Val Thr Ile Tyr Ser Phe Pro Ala Pro Asn Val Ile Leu 305 310 315	963
acg aag cca gag gtc tca gaa ggg acc gag gtg aca gtg aag tgt gag Thr Lys Pro Glu Val Ser Glu Gly Thr Glu Val Thr Val Lys Cys Glu 320 325 330	1011
gcc cac cct aga gcc aag gtg acg ctg aat ggg gtt cca gcc cag cca Ala His Pro Arg Ala Lys Val Thr Leu Asn Gly Val Pro Ala Gln Pro 335 340 345	1059
ctg ggc ccg agg gcc cag ctc ctg ctg aag gcc acc cca gag gac aac Leu Gly Pro Arg Ala Gln Leu Leu Leu Lys Ala Thr Pro Glu Asp Asn 350 355 360 365	1107
ggg cgc agc ttc tcc tgc tct gca acc ctg gag gtg gcc ggc cag ctt Gly Arg Ser Phe Ser Cys Ser Ala Thr Leu Glu Val Ala Gly Gln Leu 370 375 380	1155
ata cac aag aac cag acc cgg gag ctt cgt gtc ctg tat ggc ccc cga Ile His Lys Asn Gln Thr Arg Glu Leu Arg Val Leu Tyr Gly Pro Arg 385 390 395	1203
ctg gac gag agg gat tgt ccg gga aac tgg acg tgg cca gaa aat tcc Leu Asp Glu Arg Asp Cys Pro Gly Asn Trp Thr Trp Pro Glu Asn Ser 400 405 410	1251
cag cag act cca atg tgc cag gct tgg ggg aac cca ttg ccc gag ctc Gln Gln Thr Pro Met Cys Gln Ala Trp Gly Asn Pro Leu Pro Glu Leu 415 420 425	1299

11-88L.ST25.txt

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cgg tat gag att gtc atc atc act gtg gta gca gcc gca gtc ata atg Arg Tyr Glu Ile Val Ile Ile Thr Val Val Ala Ala Ala Val Ile Met 480 485 490	1491
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aag aaa tac aga cta caa cag gcc caa aaa ggg acc ccc atg aaa ccg Lys Lys Tyr Arg Leu Gln Gln Ala Lys Gly Thr Pro Met Lys Pro 510 515 520 525	1587
aac aca caa gcc acg cct ccc tgaacctatc ccggacagg gcctttcct Asn Thr Gln Ala Thr Pro Pro 530	1638
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<212> PRT
<213> Homo sapiens

<400> 14

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20 25 30

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35 40 45

Ser Thr Ser Cys Asp Gln Pro Lys Leu Leu Gly Ile Glu Thr Pro Leu
50 55 60

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Pro Lys Lys Glu Leu Leu Leu Pro Gly Asn Asn Arg Lys Val Tyr Glu
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Leu Ser Asn Val Gln Glu Asp Ser Gln Pro Met Cys Tyr Ser Asn Cys
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Pro Asp Gly Gln Ser Thr Ala Lys Thr Phe Leu Thr Val Tyr Trp Thr
 100 105 110

Pro Glu Arg Val Glu Leu Ala Pro Leu Pro Ser Trp Gln Pro Val Gly
 115 120 125

Lys Asn Leu Thr Leu Arg Cys Gln Val Glu Gly Gly Ala Pro Arg Ala
 130 135 140

Asn Leu Thr Val Val Leu Leu Arg Gly Glu Lys Glu Leu Lys Arg Glu
 145 150 155 160

Pro Ala Val Gly Glu Pro Ala Glu Val Thr Thr Thr Val Leu Val Arg
 165 170 175

Arg Asp His His Gly Ala Asn Phe Ser Cys Arg Thr Glu Leu Asp Leu
 180 185 190

Arg Pro Gln Gly Leu Glu Leu Phe Glu Asn Thr Ser Ala Pro Tyr Gln
 195 200 205

Leu Gln Thr Phe Val Leu Pro Ala Thr Pro Pro Gln Leu Val Ser Pro
 210 215 220

Arg Val Leu Glu Val Asp Thr Gln Gly Thr Val Val Cys Ser Leu Asp
 225 230 235 240

Gly Leu Phe Pro Val Ser Glu Ala Gln Val His Leu Ala Leu Gly Asp
 245 250 255

Gln Arg Leu Asn Pro Thr Val Thr Tyr Gly Asn Asp Ser Phe Ser Ala
 260 265 270

Lys Ala Ser Val Ser Val Thr Ala Glu Asp Glu Gly Thr Gln Arg Leu
 275 280 285

Thr Cys Ala Val Ile Leu Gly Asn Gln Ser Gln Glu Thr Leu Gln Thr
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Val Thr Ile Tyr Ser Phe Pro Ala Pro Asn Val Ile Leu Thr Lys Pro
 305 310 315 320

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Glu Val Ser Glu Gly Thr Glu Val Thr Val Lys Cys Glu Ala His Pro
325 330 335

Arg Ala Lys Val Thr Leu Asn Gly Val Pro Ala Gln Pro Leu Gly Pro
340 345 350

Arg Ala Gln Leu Leu Leu Lys Ala Thr Pro Glu Asp Asn Gly Arg Ser
355 360 365

Phe Ser Cys Ser Ala Thr Leu Glu Val Ala Gly Gln Leu Ile His Lys
370 375 380

Asn Gln Thr Arg Glu Leu Arg Val Leu Tyr Gly Pro Arg Leu Asp Glu
385 390 395 400

Arg Asp Cys Pro Gly Asn Trp Thr Trp Pro Glu Asn Ser Gln Gln Thr
405 410 415

Pro Met Cys Gln Ala Trp Gly Asn Pro Leu Pro Glu Leu Lys Cys Leu
420 425 430

Lys Asp Gly Thr Phe Pro Leu Pro Ile Gly Glu Ser Val Thr Val Thr
435 440 445

Arg Asp Leu Glu Gly Thr Tyr Leu Cys Arg Ala Arg Ser Thr Gln Gly
450 455 460

Glu Val Thr Arg Glu Val Thr Val Asn Val Leu Ser Pro Arg Tyr Glu
465 470 475 480

Ile Val Ile Ile Thr Val Val Ala Ala Ala Val Ile Met Gly Thr Ala
485 490 495

Gly Leu Ser Thr Tyr Leu Tyr Asn Arg Gln Arg Lys Ile Lys Lys Tyr
500 505 510

Arg Leu Gln Gln Ala Gln Lys Gly Thr Pro Met Lys Pro Asn Thr Gln
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530

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<211> 1921
<212> DNA
<213> Homo sapiens

<400> 15

11-88L.ST25.txt

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tgcatgtgtg taagtgtgtg tgtgtgtgtg tgtgtgtgtg tgtgtgtata catgccagtg	1860
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11-88L.ST25.txt

a

1921

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<211> 1476
<212> DNA
<213> Homo sapiens

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ggggaggcat tatgtatatt atttccggat cactcctggc agcaacggag aaaaactcca	420
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ctggaatgtatc ttttcaatc atggacatac ttaatattaa aatttcccat tttttaaaaa	540
tggagagtct gaattttatt agagtcaca caccatatat taacatatac aactgtgaac	600
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tgttcttggg cattttgtca gtgatgctga tctttgcctt cttccaggaa cttgtatag	720
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<210> 17
<211> 2290

11-88L.ST25.txt

<212> DNA
 <213> Homo sapiens

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11-88L.ST25.txt

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<212> DNA
<213> Homo sapiens

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11-88L.ST25.txt

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 <212> DNA
 <213> Homo sapiens

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11-88L.ST25.txt

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<210> 20
<211> 1870
<212> DNA
<213> *Homo sapiens*

<220>
<221> CDS
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Met Gly Cys Asp Arg Asn Cys Gly
1 5

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 Leu Ile Ala Gly Ala Val Ile Gly Ala Val Leu Ala Val Phe Gly Gly
 10 15 20

att cta atg cca gtt gga gac ctg ctt atc cag aag aca att aaa aag 330
 Ile Leu Met Pro Val Gly Asp Leu Leu Ile Gln Lys Thr Ile Lys Lys
 25 30 35 40

caa gtt gtc ctc gaa gaa ggt aca att gct ttt aaa aat tgg gtt aaa 378
 Gln Val Val Leu Glu Glu Gly Thr Ile Ala Phe Lys Asn Trp Val Lys
 45 50 55

aca ggc aca gaa gtt tac aga cag ttt tgg atc ttt gat gtg caa aat 426
 Thr Gly Thr Glu Val Tyr Arg Gln Phe Trp Ile Phe Asp Val Gln Asn
 60 65 70

cca cag gaa gtg atg atg aac agc agc aac att caa gtt aag caa aga 474
 Pro Gln Glu Val Met Met Asn Ser Ser Asn Ile Gln Val Lys Gln Arg
 75 80 85

ggt cct tat acg tac aga gtt cgt ttt cta gcc aag gaa aat gta acc 522
Gly Pro Tyr Thr Tyr Arg Val Arg Phe Leu Ala Lys Glu Asn Val Thr
90 95 100

cag gac gct gag gac aac aca gtc tct ttc ctg cag ccc aat ggt gcc
Gln Asp Ala Glu Asp Asn Thr Val Ser Phe Leu Gln Pro Asn Gly Ala 570

11-88L.ST25.txt

105	110	115	120	
atc ttc gaa cct tca cta tca gtt gga aca gag gct gac aac ttc aca Ile Phe Glu Pro Ser Leu Ser Val Gly Thr Glu Ala Asp Asn Phe Thr 125		130	135	618
gtt ctc aat ctg gct gtg gca gct gca tcc cat atc tat caa aat caa Val Leu Asn Leu Ala Val Ala Ala Ser His Ile Tyr Gln Asn Gln 140	145		150	666
ttt gtt caa atg atc ctc aat tca ctt att aac aag tca aaa tct tct Phe Val Gln Met Ile Leu Asn Ser Leu Ile Asn Lys Ser Lys Ser Ser 155	160	165		714
atg ttc caa gtc aga act ttg aga gaa ctg tta tgg ggc tat agg gat Met Phe Gln Val Arg Thr Leu Arg Glu Leu Leu Trp Gly Tyr Arg Asp 170	175	180		762
cca ttt ttg agt ttg gtt ccg tac cct gtt act acc aca gtt ggt ctg Pro Phe Leu Ser Leu Val Pro Tyr Pro Val Thr Thr Thr Val Gly Leu 185	190	195	200	810
ttt tat cct tac aac aat act gca gat gga gtt tat aaa gtt ttc aat Phe Tyr Pro Tyr Asn Asn Thr Ala Asp Gly Val Tyr Lys Val Phe Asn 205	210		215	858
gga aaa gat aac ata agt aaa gtt gcc ata atc gac aca tat aaa ggt Gly Lys Asp Asn Ile Ser Lys Val Ala Ile Ile Asp Thr Tyr Lys Gly 220	225		230	906
aaa agg aat ctg tcc tat tgg gaa agt cac tgc gac atg att aat ggt Lys Arg Asn Leu Ser Tyr Trp Glu Ser His Cys Asp Met Ile Asn Gly 235	240		245	954
aca gat gca gcc tca ttt cca cct ttt gtt gag aaa agc cag gta ttg Thr Asp Ala Ala Ser Phe Pro Pro Phe Val Glu Lys Ser Gln Val Leu 250	255	260		1002
cag ttc ttt tct tct gat att tgc agg tca atc tat gct gta ttt gaa Gln Phe Phe Ser Ser Asp Ile Cys Arg Ser Ile Tyr Ala Val Phe Glu 265	270	275	280	1050
tcc gac gtt aat ctg aaa gga atc cct gtg tat aga ttt gtt ctt cca Ser Asp Val Asn Leu Lys Gly Ile Pro Val Tyr Arg Phe Val Leu Pro 285	290		295	1098
tcc aag gcc ttt gcc tct cca gtt gaa aac cca gac aac tat tgt ttc Ser Lys Ala Phe Ala Ser Pro Val Glu Asn Pro Asp Asn Tyr Cys Phe 300	305		310	1146
tgc aca gaa aaa att atc tca aaa aat tgt aca tca tat ggt gtg cta Cys Thr Glu Lys Ile Ile Ser Lys Asn Cys Thr Ser Tyr Gly Val Leu 315	320	325		1194
gac atc agc aaa tgc aaa gaa ggg aga cct gtg tac att tca ctt cct Asp Ile Ser Lys Cys Lys Glu Gly Arg Pro Val Tyr Ile Ser Leu Pro 330	335	340		1242
cat ttt ctg tat gca agt cct gat gtt tca gaa cct att gat gga tta His Phe Leu Tyr Ala Ser Pro Asp Val Ser Glu Pro Ile Asp Gly Leu 345	350	355	360	1290
aac cca aat gaa gaa cat agg aca tac ttg gat att gaa cct ata				1338

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Asn Pro Asn Glu Glu Glu His Arg Thr Tyr Leu Asp Ile Glu Pro Ile			
365	370	375	
act gga ttc act tta caa ttt gca aaa cgg ctg cag gtc aac cta ttg			1386
Thr Gly Phe Thr Leu Gln Phe Ala Lys Arg Leu Gln Val Asn Leu Leu			
380	385	390	
gtc aag cca tca gaa aaa att caa gta tta aag aat ctg aag agg aac			1434
Val Lys Pro Ser Glu Lys Ile Gln Val Leu Lys Asn Leu Lys Arg Asn			
395	400	405	
tat att gtg cct att ctt tgg ctt aat gag act ggg acc att ggt gat			1482
Tyr Ile Val Pro Ile Leu Trp Leu Asn Glu Thr Gly Thr Ile Gly Asp			
410	415	420	
gag aag gca aac atg ttc aga agt caa gta act gga aaa ata aac ctc			1530
Glu Lys Ala Asn Met Phe Arg Ser Gln Val Thr Gly Lys Ile Asn Leu			
425	430	435	440
ctt ggc ctg ata gaa atg atc tta ctc agt gtt ggt gtg gtg atg ttt			1578
Leu Gly Leu Ile Glu Met Ile Leu Leu Ser Val Gly Val Val Met Phe			
445	450	455	
gtt gct ttt atg att tca tat tgt gca tgc aga tcg aaa aca ata aaa			1626
Val Ala Phe Met Ile Ser Tyr Cys Ala Cys Arg Ser Lys Thr Ile Lys			
460	465	470	
taagtatgta ccaaaaata ttgcttcaat aatattagct tatatatattac ttgtttcac			1686
tttatcaaag agaagttaca tattaggcca tatatatattc tagacatgtc tagccactga			1746
tcattttaa atataggtaa ataaacctat aaatattatc acgcagatca ctaaagtata			1806
tcttaattc tgggagaaaat gagataaaag atgtacttgt gaccattgta acaatagcac			1866
aaat			1870

<210> 21
<211> 472
<212> PRT
<213> Homo sapiens

<400> 21

Met Gly Cys Asp Arg Asn Cys Gly Leu Ile Ala Gly Ala Val Ile Gly
1 5 10 15

Ala Val Leu Ala Val Phe Gly Gly Ile Leu Met Pro Val Gly Asp Leu
20 25 30

Leu Ile Gln Lys Thr Ile Lys Lys Gln Val Val Leu Glu Glu Gly Thr
35 40 45

Ile Ala Phe Lys Asn Trp Val Lys Thr Gly Thr Glu Val Tyr Arg Gln
50 55 60

Phe Trp Ile Phe Asp Val Gln Asn Pro Gln Glu Val Met Met Asn Ser
65 70 75 80

11-88L.ST25.txt

Ser Asn Ile Gln Val Lys Gln Arg Gly Pro Tyr Thr Tyr Arg Val Arg
85 90 95

Phe Leu Ala Lys Glu Asn Val Thr Gln Asp Ala Glu Asp Asn Thr Val
100 105 110

Ser Phe Leu Gln Pro Asn Gly Ala Ile Phe Glu Pro Ser Leu Ser Val
115 120 125

Gly Thr Glu Ala Asp Asn Phe Thr Val Leu Asn Leu Ala Val Ala Ala
130 135 140

Ala Ser His Ile Tyr Gln Asn Gln Phe Val Gln Met Ile Leu Asn Ser
145 150 155 160

Leu Ile Asn Lys Ser Lys Ser Ser Met Phe Gln Val Arg Thr Leu Arg
165 170 175

Glu Leu Leu Trp Gly Tyr Arg Asp Pro Phe Leu Ser Leu Val Pro Tyr
180 185 190

Pro Val Thr Thr Thr Val Gly Leu Phe Tyr Pro Tyr Asn Asn Thr Ala
195 200 205

Asp Gly Val Tyr Lys Val Phe Asn Gly Lys Asp Asn Ile Ser Lys Val
210 215 220

Ala Ile Ile Asp Thr Tyr Lys Gly Lys Arg Asn Leu Ser Tyr Trp Glu
225 230 235 240

Ser His Cys Asp Met Ile Asn Gly Thr Asp Ala Ala Ser Phe Pro Pro
245 250 255

Phe Val Glu Lys Ser Gln Val Leu Gln Phe Phe Ser Ser Asp Ile Cys
260 265 270

Arg Ser Ile Tyr Ala Val Phe Glu Ser Asp Val Asn Leu Lys Gly Ile
275 280 285

Pro Val Tyr Arg Phe Val Leu Pro Ser Lys Ala Phe Ala Ser Pro Val
290 295 300

Glu Asn Pro Asp Asn Tyr Cys Phe Cys Thr Glu Lys Ile Ile Ser Lys
305 310 315 320

Asn Cys Thr Ser Tyr Gly Val Leu Asp Ile Ser Lys Cys Lys Glu Gly
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325

330

335

Arg Pro Val Tyr Ile Ser Leu Pro His Phe Leu Tyr Ala Ser Pro Asp
 340 345 350

Val Ser Glu Pro Ile Asp Gly Leu Asn Pro Asn Glu Glu Glu His Arg
 355 360 365

Thr Tyr Leu Asp Ile Glu Pro Ile Thr Gly Phe Thr Leu Gln Phe Ala
 370 375 380

Lys Arg Leu Gln Val Asn Leu Leu Val Lys Pro Ser Glu Lys Ile Gln
 385 390 395 400

Val Leu Lys Asn Leu Lys Arg Asn Tyr Ile Val Pro Ile Leu Trp Leu
 405 410 415

Asn Glu Thr Gly Thr Ile Gly Asp Glu Lys Ala Asn Met Phe Arg Ser
 420 425 430

Gln Val Thr Gly Lys Ile Asn Leu Leu Gly Leu Ile Glu Met Ile Leu
 435 440 445

Leu Ser Val Gly Val Val Met Phe Val Ala Phe Met Ile Ser Tyr Cys
 450 455 460

Ala Cys Arg Ser Lys Thr Ile Lys
 465 470

<210> 22
<211> 1321
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (37)..(1158)

<400> 22
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Met Trp Phe Leu Thr Thr
1 5

ctg ctc ctt tgg gtt cca gtt gat ggg caa gtg gac acc aca aag gca 102
Leu Leu Leu Trp Val Pro Val Asp Gly Gln Val Asp Thr Thr Lys Ala
10 15 20

gtg atc tct ttg cag cct cca tgg gtc agc gtg ttc caa gag gaa acc 150
Val Ile Ser Leu Gln Pro Pro Trp Val Ser Val Phe Gln Glu Glu Thr
25 30 35

gta acc ttg cac tgt gag gtg ctc cat ctg cct ggg agc agc tct aca 198

11-88L.ST25.txt

val Thr Leu His Cys Glu Val Leu His Leu Pro Gly Ser Ser Ser Thr			
40	45	50	
cag tgg ttt ctc aat ggc aca gcc act cag acc tcg acc ccc agc tac			246
Gln Trp Phe Leu Asn Gly Thr Ala Thr Gln Thr Ser Thr Pro Ser Tyr			
55	60	65	70
aga atc acc tct gcc agt gtc aat gac agt ggt gaa tac agg tgc cag			294
Arg Ile Thr Ser Ala Ser Val Asn Asp Ser Gly Glu Tyr Arg Cys Gln			
75	80	85	
aga ggt ctc tca ggg cga agt gac ccc ata cag ctg gaa atc cac aga			342
Arg Gly Leu Ser Gly Arg Ser Asp Pro Ile Gln Leu Glu Ile His Arg			
90	95	100	
ggc tgg cta cta ctg cag gtc tcc agc aga gtc ttc acg gaa gga gaa			390
Gly Trp Leu Leu Leu Gln Val Ser Ser Arg Val Phe Thr Glu Gly Glu			
105	110	115	
cct ctg gcc ttg agg tgt cat gcg tgg aag gat aag ctg gtg tac aat			438
Pro Leu Ala Leu Arg Cys His Ala Trp Lys Asp Lys Leu Val Tyr Asn			
120	125	130	
gtg ctt tac tat cga aat ggc aaa gcc ttt aag ttt ttc cac tgg aat			486
Val Leu Tyr Tyr Arg Asn Gly Lys Ala Phe Lys Phe Phe His Trp Asn			
135	140	145	150
tct aac ctc acc att ctg aaa acc aac ata agt cac aat ggc acc tac			534
Ser Asn Leu Thr Ile Leu Lys Thr Asn Ile Ser His Asn Gly Thr Tyr			
155	160	165	
cat tgc tca ggc atg gga aag cat cgc tac aca tca gca gga ata tct			582
His Cys Ser Gly Met Gly Lys His Arg Tyr Thr Ser Ala Gly Ile Ser			
170	175	180	
gtc act gtg aaa gag cta ttt cca gct cca gtg ctg aat gca tct gtg			630
Val Thr Val Lys Glu Leu Phe Pro Ala Pro Val Leu Asn Ala Ser Val			
185	190	195	
aca tcc cca ctc ctg gag ggg aat ctg gtc acc ctg agc tgt gaa aca			678
Thr Ser Pro Leu Leu Glu Gly Asn Leu Val Thr Leu Ser Cys Glu Thr			
200	205	210	
aag ttg ctc ttg cag agg cct ggt ttg cag ctt tac ttc tcc ttc tac			726
Lys Leu Leu Leu Gln Arg Pro Gly Leu Gln Leu Tyr Phe Ser Phe Tyr			
215	220	225	230
atg ggc agc aag acc ctg cga ggc agg aac aca tcc tct gaa tac caa			774
Met Gly Ser Lys Thr Leu Arg Gly Arg Asn Thr Ser Ser Glu Tyr Gln			
235	240	245	
ata cta act gct aga aga gaa gac tct ggg tta tac tgg tgc gag gct			822
Ile Leu Thr Ala Arg Arg Glu Asp Ser Gly Leu Tyr Trp Cys Glu Ala			
250	255	260	
gcc aca gag gat gga aat gtc ctt aag cgc agc cct gag ttg gag ctt			870
Ala Thr Glu Asp Gly Asn Val Leu Lys Arg Ser Pro Glu Leu Glu Leu			
265	270	275	
caa gtg ctt ggc ctc cag tta cca act cct gtc tgg ttt cat gtc ctt			918
Gln Val Leu Gly Leu Gln Leu Pro Thr Pro Val Trp Phe His Val Leu			
280	285	290	

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ttc tat ctg gca gtg gga ata atg ttt tta gtg aac act gtt ctc tgg Phe Tyr Leu Ala Val Gly Ile Met Phe Leu Val Asn Thr Val Leu Trp 295 300 305 310	966
gtg aca ata cgt aaa gaa ctg aaa aga aag aaa aag tgg gat tta gaa Val Thr Ile Arg Lys Glu Leu Lys Arg Lys Lys Trp Asp Leu Glu 315 320 325	1014
atc tct ttg gat tct ggt cat gag aag aag gta act tcc agc ctt caa Ile Ser Leu Asp Ser Gly His Glu Lys Lys Val Thr Ser Ser Leu Gln 330 335 340	1062
gaa gac aga cat tta gaa gaa gag ctg aaa tgt cag gaa caa aaa gaa Glu Asp Arg His Leu Glu Glu Leu Lys Cys Gln Glu Gln Lys Glu 345 350 355	1110
gaa cag ctg cag gaa ggg gtg cac cgg aag gag ccc cag ggg gcc acg Glu Gln Leu Gln Glu Gly Val His Arg Lys Glu Pro Gln Gly Ala Thr 360 365 370	1158
tagcagcggc tcagtgggtg gccatcgatc tggaccgtcc cctgcccact tgctccccgt	1218
gagcactgcg tacaaacatc caaaagttca acaacaccag aactgtgtgt ctcatggtat	1278
gtaactctta aagcaaataa atgaactgac ttcaaaaaaaa aaa	1321

<210> 23
<211> 374
<212> PRT
<213> Homo sapiens

<400> 23

Met Trp Phe Leu Thr Thr Leu Leu Leu Trp Val Pro Val Asp Gly Gln
1 5 10 15

Val Asp Thr Thr Lys Ala Val Ile Ser Leu Gln Pro Pro Trp Val Ser
20 25 30

Val Phe Gln Glu Glu Thr Val Thr Leu His Cys Glu Val Leu His Leu
35 40 45

Pro Gly Ser Ser Ser Thr Gln Trp Phe Leu Asn Gly Thr Ala Thr Gln
50 55 60

Thr Ser Thr Pro Ser Tyr Arg Ile Thr Ser Ala Ser Val Asn Asp Ser
65 70 75 80

Gly Glu Tyr Arg Cys Gln Arg Gly Leu Ser Gly Arg Ser Asp Pro Ile
85 90 95

Gln Leu Glu Ile His Arg Gly Trp Leu Leu Leu Gln Val Ser Ser Arg
100 105 110

Val Phe Thr Glu Gly Glu Pro Leu Ala Leu Arg Cys His Ala Trp Lys
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115

120

125

Asp Lys Leu val Tyr Asn Val Leu Tyr Tyr Arg Asn Gly Lys Ala Phe
 130 135 140

Lys Phe Phe His Trp Asn Ser Asn Leu Thr Ile Leu Lys Thr Asn Ile
 145 150 155 160

Ser His Asn Gly Thr Tyr His Cys Ser Gly Met Gly Lys His Arg Tyr
 165 170 175

Thr Ser Ala Gly Ile Ser Val Thr Val Lys Glu Leu Phe Pro Ala Pro
 180 185 190

Val Leu Asn Ala Ser Val Thr Ser Pro Leu Leu Glu Gly Asn Leu Val
 195 200 205

Thr Leu Ser Cys Glu Thr Lys Leu Leu Leu Gln Arg Pro Gly Leu Gln
 210 215 220

Leu Tyr Phe Ser Phe Tyr Met Gly Ser Lys Thr Leu Arg Gly Arg Asn
 225 230 235 240

Thr Ser Ser Glu Tyr Gln Ile Leu Thr Ala Arg Arg Glu Asp Ser Gly
 245 250 255

Leu Tyr Trp Cys Glu Ala Ala Thr Glu Asp Gly Asn Val Leu Lys Arg
 260 265 270

Ser Pro Glu Leu Glu Leu Gln Val Leu Gly Leu Gln Leu Pro Thr Pro
 275 280 285

Val Trp Phe His Val Leu Phe Tyr Leu Ala Val Gly Ile Met Phe Leu
 290 295 300

Val Asn Thr Val Leu Trp Val Thr Ile Arg Lys Glu Leu Lys Arg Lys
 305 310 315 320

Lys Lys Trp Asp Leu Glu Ile Ser Leu Asp Ser Gly His Glu Lys Lys
 325 330 335

Val Thr Ser Ser Leu Gln Glu Asp Arg His Leu Glu Glu Leu Lys
 340 345 350

Cys Gln Glu Gln Lys Glu Glu Gln Leu Gln Glu Gly Val His Arg Lys
 355 360 365

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Glu Pro Gln Gly Ala Thr
370

<210> 24
<211> 1714
<212> DNA
<213> *Homo sapiens*

<220>
<221> CDS
<222> (156)..(1163)

11-88L.ST25.txt

aag atc cag ccc cgt cag atc gac ctc tta act tac tgc aac ttg gtc Lys Ile Gln Pro Arg Gln Ile Asp Leu Leu Thr Tyr Cys Asn Leu Val 170 175 180	701
cat ggc aga aat ttc acc tcc aag ttc cca aga caa ata gtg agc aac His Gly Arg Asn Phe Thr Ser Lys Phe Pro Arg Gln Ile Val Ser Asn 185 190 195	749
tgc agc cac gga agg tgg agc gtc atc gtc atc ccc gat gtc aca gtc Cys Ser His Gly Arg Trp Ser Val Ile Val Ile Pro Asp Val Thr Val 200 205 210	797
tca gac tcg ggg ctt tac cgc tgc tac ttg cag gcc agc gca gga gaa Ser Asp Ser Gly Leu Tyr Arg Cys Tyr Leu Gln Ala Ser Ala Gly Glu 215 220 225 230	845
aac gaa acc ttc gtg atg aga ttg act gta gcc gag ggt aaa acc gat Asn Glu Thr Phe Val Met Arg Leu Thr Val Ala Glu Gly Lys Thr Asp 235 240 245	893
aac caa tat acc ctc ttt gtg gct gga ggg aca gtt tta ttg ttg ttg Asn Gln Tyr Thr Leu Phe Val Ala Gly Gly Thr Val Leu Leu Leu Leu 250 255 260	941
ttt gtt atc tca att acc acc atc att gtc att ttc ctt aac aga agg Phe Val Ile Ser Ile Thr Thr Ile Ile Val Ile Phe Leu Asn Arg Arg 265 270 275	989
aga agg aga gag aga aga gat cta ttt aca gag tcc tgg gat aca cag Arg Arg Arg Glu Arg Arg Asp Leu Phe Thr Glu Ser Trp Asp Thr Gln 280 285 290	1037
aag gca ccc aat aac tat aga agt ccc atc tct acc ggt caa cct acc Lys Ala Pro Asn Asn Tyr Arg Ser Pro Ile Ser Thr Gly Gln Pro Thr 295 300 305 310	1085
aat caa tcc atg gat gat aca aga gag gat att tat gtc aac tat cca Asn Gln Ser Met Asp Asp Thr Arg Glu Asp Ile Tyr Val Asn Tyr Pro 315 320 325	1133
acc ttc tct cgc aga cca aag act aga gtt taagcttatt cttgacatga Thr Phe Ser Arg Arg Pro Lys Thr Arg Val 330 335	1183
gtgcattagt aatgactctt atgtactcat gcatggatct ttatgcaatt tttttccact	1243
acccaaggc taccttagat actagttgtc tgaatttgagt tactttgata ggaaaaatac	1303
ttcattacct aaaatcattt ttcatagaac tgttcagaa aacctgactc taactggttt	1363
atatacaaaa gaaaacttac tgtatcatat aacagaatga tccaggggag attaagcttt	1423
ggccaaggc tatattaccag ggcttaaatg ttgtgtctag aattaagtat gggcataaac	1483
tggcttctga atccccttcc agagtgttgg atccatttcc ctggcttgg cctcactctc	1543
atgcaggctt tcctcttgtt ttggcaagat ggctgccaac tcttggcaat tcatacatcc	1603
ttgtttctgt ctggtagaga gtttgcttct caaatggagc aaacaaattt gattatTTT	1663
tcattgttaa ataggcaaca tgaccataaa ggatggaatg gcttaagtaa a	1714

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<210> 25
<211> 336
<212> PRT
<213> Homo sapiens

<400> 25

Met Asp Tyr Pro Thr Leu Leu Leu Ala Leu Leu His Val Tyr Arg Ala
1 5 10 15

Leu Cys Glu Glu Val Leu Trp His Thr Ser Val Pro Phe Ala Glu Asn
20 25 30

Met Ser Leu Glu Cys Val Tyr Pro Ser Met Gly Ile Leu Thr Gln Val
35 40 45

Glu Trp Phe Lys Ile Gly Thr Gln Gln Asp Ser Ile Ala Ile Phe Ser
50 55 60

Pro Thr His Gly Met Val Ile Arg Lys Pro Tyr Ala Glu Arg Val Tyr
65 70 75 80

Phe Leu Asn Ser Thr Met Ala Ser Asn Asn Met Thr Leu Phe Phe Arg
85 90 95

Asn Ala Ser Glu Asp Asp Val Gly Tyr Tyr Ser Cys Ser Leu Tyr Thr
100 105 110

Tyr Pro Gln Gly Thr Trp Gln Lys Val Ile Gln Val Val Gln Ser Asp
115 120 125

Ser Phe Glu Ala Ala Val Pro Ser Asn Ser His Ile Val Ser Glu Pro
130 135 140

Gly Lys Asn Val Thr Leu Thr Cys Gln Pro Gln Met Thr Trp Pro Val
145 150 155 160

Gln Ala Val Arg Trp Glu Lys Ile Gln Pro Arg Gln Ile Asp Leu Leu
165 170 175

Thr Tyr Cys Asn Leu Val His Gly Arg Asn Phe Thr Ser Lys Phe Pro
180 185 190

Arg Gln Ile Val Ser Asn Cys Ser His Gly Arg Trp Ser Val Ile Val
195 200 205

Ile Pro Asp Val Thr Val Ser Asp Ser Gly Leu Tyr Arg Cys Tyr Leu
210 215 220

11-88L.ST25.txt

Gln Ala Ser Ala Gly Glu Asn Glu Thr Phe Val Met Arg Leu Thr Val
 225 230 235 240

Ala Glu Gly Lys Thr Asp Asn Gln Tyr Thr Leu Phe Val Ala Gly Gly
 245 250 255

Thr Val Leu Leu Leu Phe Val Ile Ser Ile Thr Thr Ile Ile Val
 260 265 270

Ile Phe Leu Asn Arg Arg Arg Arg Glu Arg Arg Asp Leu Phe Thr
 275 280 285

Glu Ser Trp Asp Thr Gln Lys Ala Pro Asn Asn Tyr Arg Ser Pro Ile
 290 295 300

Ser Thr Gly Gln Pro Thr Asn Gln Ser Met Asp Asp Thr Arg Glu Asp
 305 310 315 320

Ile Tyr Val Asn Tyr Pro Thr Phe Ser Arg Arg Pro Lys Thr Arg Val
 325 330 335

<210> 26

<211> 2107

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (35)..(1975)

<400> 26

acgcggaaac aggcttgcac ccagacacga cacc atg cat ctc ctc ggc ccc tgg 55
 Met His Leu Leu Gly Pro Trp
 1 5

ctc ctg ctc ctg gtt cta gaa tac ttg gct ttc tct gac tca agt aaa 103
 Leu Leu Leu Val Leu Glu Tyr Leu Ala Phe Ser Asp Ser Ser Lys
 10 15 20

tgg gtt ttt gag cac cct gaa acc ctc tac gcc tgg gag ggg gcc tgc 151
 Trp Val Phe Glu His Pro Glu Thr Leu Tyr Ala Trp Glu Gly Ala Cys
 25 30 35

gtc tgg atc ccc tgc acc tac aga gcc cta gat ggt gac ctg gaa agc 199
 Val Trp Ile Pro Cys Thr Tyr Arg Ala Leu Asp Gly Asp Leu Glu Ser
 40 45 50 55

ttc atc ctg ttc cac aat cct gag tat aac aag aac acc tcg aag ttt 247
 Phe Ile Leu Phe His Asn Pro Glu Tyr Asn Lys Asn Thr Ser Lys Phe
 60 65 70

gat ggg aca aga ctc tat gaa agc aca aag gat ggg aag gtt cct tct 295
 Asp Gly Thr Arg Leu Tyr Glu Ser Thr Lys Asp Gly Lys Val Pro Ser
 75 80 85

11-88L.ST25.txt

gag cag aaa agg gtg caa ttc ctg gga gac aag aat aag aac tgc aca Glu Gln Lys Arg Val Gln Phe Leu Gly Asp Lys Asn Lys Asn Cys Thr 90 95 100	343
ctg agt atc cac ccg gtg cac ctc aat gac agt ggt cag ctg ggg ctg Leu Ser Ile His Pro Val His Leu Asn Asp Ser Gly Gln Leu Gly Leu 105 110 115	391
agg atg gag tcc aag act gag aaa tgg atg gaa cga ata cac ctc aat Arg Met Glu Ser Lys Thr Glu Lys Trp Met Glu Arg Ile His Leu Asn 120 125 130 135	439
gtc tct gaa agg cct ttt cca cct cat atc cag ctc cct cca gaa att Val Ser Glu Arg Pro Phe Pro His Ile Gln Leu Pro Pro Glu Ile 140 145 150	487
caa gag tcc cag gaa gtc act ctg acc tgc ttg ctg aat ttc tcc tgc Gln Glu Ser Gln Glu Val Thr Leu Thr Cys Leu Leu Asn Phe Ser Cys 155 160 165	535
tat ggg tat ccg atc caa ttg cag tgg ctc cta gag ggg gtt cca atg Tyr Gly Tyr Pro Ile Gln Leu Gln Trp Leu Leu Glu Gly Val Pro Met 170 175 180	583
agg cag gct gtc acc tcg acc tcc ttg acc atc aag tct gtc ttc Arg Gln Ala Ala Val Thr Ser Thr Ser Leu Thr Ile Lys Ser Val Phe 185 190 195	631
acc cgg agc gag ctc aag ttc tcc cca cag tgg agt cac cat ggg aag Thr Arg Ser Glu Leu Lys Phe Ser Pro Gln Trp Ser His His Gly Lys 200 205 210 215	679
att gtg acc tgc cag ctt cag gat gca gat ggg aag ttc ctc tcc aat Ile Val Thr Cys Gln Leu Gln Asp Ala Asp Gly Lys Phe Leu Ser Asn 220 225 230	727
gac acg gtg cag ctg aac gtg aag cat cct ccc aag aag gtg acc aca Asp Thr Val Gln Leu Asn Val Lys His Pro Pro Lys Lys Val Thr Thr 235 240 245	775
gtg att caa aac ccc atg ccg att cga gaa gga gac aca gtg acc ctt Val Ile Gln Asn Pro Met Pro Ile Arg Glu Gly Asp Thr Val Thr Leu 250 255 260	823
tcc tgt aac tac aat tcc agt aac ccc agt gtt acc cggt tat gaa tgg Ser Cys Asn Tyr Asn Ser Ser Asn Pro Ser Val Thr Arg Tyr Glu Trp 265 270 275	871
aaa ccc cat ggc gcc tgg gag gag cca tcg ctt ggg gtg ctg aag atc Lys Pro His Gly Ala Trp Glu Glu Pro Ser Leu Gly Val Leu Lys Ile 280 285 290 295	919
caa aac gtt ggc tgg gac aac aca acc atc gcc tgc gca gct tgt aat Gln Asn Val Gly Trp Asp Asn Thr Thr Ile Ala Cys Ala Ala Cys Asn 300 305 310	967
agt tgg tgc tcg tgg gcc tcc cct gtc gcc ctg aat gtc cag tat gcc Ser Trp Cys Ser Trp Ala Ser Pro Val Ala Leu Asn Val Gln Tyr Ala 315 320 325	1015
ccc cga gac gtg agg gtc cggt aaa atc aag ccc ctt tcc gag att cac Pro Arg Asp Val Arg Val Arg Lys Ile Lys Pro Leu Ser Glu Ile His 330 335 340	1063

11-88L.ST25.txt

tct gga aac tcg gtc agc ctc caa tgt gac ttc tca agc agc cac ccc Ser Gly Asn Ser Val Ser Leu Gln Cys Asp Phe Ser Ser Ser His Pro 345 350 355	1111
aaa gaa gtc cag ttc ttc tgg gag aaa aat ggc agg ctt ctg ggg aaa Lys Glu Val Gln Phe Phe Trp Glu Lys Asn Gly Arg Leu Leu Gly Lys 360 365 370 375	1159
gaa agc cag ctg aat ttt gac tcc atc tcc cca gaa gat gct ggg agt Glu Ser Gln Leu Asn Phe Asp Ser Ile Ser Pro Glu Asp Ala Gly Ser 380 385 390	1207
tac agc tgc tgg gtg aac aac tcc ata gga cag aca gcg tcc aag gcc Tyr Ser Cys Trp Val Asn Asn Ser Ile Gly Gln Thr Ala Ser Lys Ala 395 400 405	1255
tgg aca ctt gaa gtg ctg tat gca ccc agg agg ctg cgt gtg tcc atg Trp Thr Leu Glu Val Leu Tyr Ala Pro Arg Arg Leu Arg Val Ser Met 410 415 420	1303
agc ccg ggg gac caa gtg atg gag ggg aag agt gca acc ctg acc tgt Ser Pro Gly Asp Gln Val Met Glu Gly Lys Ser Ala Thr Leu Thr Cys 425 430 435	1351
gag agc gac gcc aac cct ccc gtc tcc cac tac acc tgg ttt gac tgg Glu Ser Asp Ala Asn Pro Pro Val Ser His Tyr Thr Trp Phe Asp Trp 440 445 450 455	1399
aat aac caa agc ctc ccc tac cac agc cag aag ctg aga ttg gag ccg Asn Asn Gln Ser Leu Pro Tyr His Ser Gln Lys Leu Arg Leu Glu Pro 460 465 470	1447
gtg aag gtc cag cac tcg ggt gcc tac tgg tgc cag ggg acc aac agt Val Lys Val Gln His Ser Gly Ala Tyr Trp Cys Gln Gly Thr Asn Ser 475 480 485	1495
gtg ggc aag ggc cgt tcg cct ctc agc acc ctc acc gtc tac tat agc Val Gly Lys Gly Arg Ser Pro Leu Ser Thr Leu Thr Val Tyr Tyr Ser 490 495 500	1543
ccg gag acc atc ggc agg cga gtg gct gtg gga ctc ggg tcc tgc ctc Pro Glu Thr Ile Gly Arg Arg Val Ala Val Gly Leu Gly Ser Cys Leu 505 510 515	1591
gcc atc ctc atc ctg gca atc tgt ggg ctc aag ctc cag cga cgt tgg Ala Ile Leu Ile Leu Ala Ile Cys Gly Leu Lys Leu Gln Arg Arg Trp 520 525 530 535	1639
aag agg aca cag agc cag cag ggg ctt cag gag aat tcc agc ggc cag Lys Arg Thr Gln Ser Gln Gln Gly Leu Gln Glu Asn Ser Ser Gly Gln 540 545 550	1687
agc ttc ttt gtg agg aat aaa aag gtt aga agg gcc ccc ctc tct gaa Ser Phe Phe Val Arg Asn Lys Lys Val Arg Arg Ala Pro Leu Ser Glu 555 560 565	1735
ggc ccc cac tcc ctg gga tgc tac aat cca atg atg gaa gat ggc att Gly Pro His Ser Leu Gly Cys Tyr Asn Pro Met Met Glu Asp Gly Ile 570 575 580	1783
agc tac acc acc ctg cgc ttt ccc gag atg aac ata cca cga act gga Ser Tyr Thr Thr Leu Arg Phe Pro Glu Met Asn Ile Pro Arg Thr Gly	1831

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585

590

595

gat gca gag tcc tca gag atg cag aga cct ccc ccg gac tgc gat gac 1879
 Asp Ala Glu Ser Ser Glu Met Gln Arg Pro Pro Pro Asp Cys Asp Asp
 600 605 610 615

acg gtc act tat tca gca ttg cac aag cgc caa gtg ggc act atg aga 1927
 Thr Val Thr Tyr Ser Ala Leu His Lys Arg Gln Val Gly Thr Met Arg
 620 625 630

acg tca ttc cag att ttc cag aag atg agg gga ttc att act cag agc 1975
 Thr Ser Phe Gln Ile Phe Gln Lys Met Arg Gly Phe Ile Thr Gln Ser
 635 640 645

tgatccagtt tgggtcggg gagcggcctc aggcacaaga aaatgtggac tatgtgatcc 2035

tcaaacattg acactggatg ggctgcagca gaggcactgg gggcagcggg ggccaggaa 2095

gtccccgagt tt 2107

<210> 27

<211> 647

<212> PRT

<213> Homo sapiens

<400> 27

Met His Leu Leu Gly Pro Trp Leu Leu Leu Leu Val Leu Glu Tyr Leu
 1 5 10 15

Ala Phe Ser Asp Ser Ser Lys Trp Val Phe Glu His Pro Glu Thr Leu
 20 25 30

Tyr Ala Trp Glu Gly Ala Cys Val Trp Ile Pro Cys Thr Tyr Arg Ala
 35 40 45

Leu Asp Gly Asp Leu Glu Ser Phe Ile Leu Phe His Asn Pro Glu Tyr
 50 55 60

Asn Lys Asn Thr Ser Lys Phe Asp Gly Thr Arg Leu Tyr Glu Ser Thr
 65 70 75 80

Lys Asp Gly Lys Val Pro Ser Glu Gln Lys Arg Val Gln Phe Leu Gly
 85 90 95

Asp Lys Asn Lys Asn Cys Thr Leu Ser Ile His Pro Val His Leu Asn
 100 105 110

Asp Ser Gly Gln Leu Gly Leu Arg Met Glu Ser Lys Thr Glu Lys Trp
 115 120 125

Met Glu Arg Ile His Leu Asn Val Ser Glu Arg Pro Phe Pro Pro His
 130 135 140

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Ile Gln Leu Pro Pro Glu Ile Gln Glu Ser Gln Glu Val Thr Leu Thr
145 150 155 160

Cys Leu Leu Asn Phe Ser Cys Tyr Gly Tyr Pro Ile Gln Leu Gln Trp
165 170 175

Leu Leu Glu Gly Val Pro Met Arg Gln Ala Ala Val Thr Ser Thr Ser
180 185 190

Leu Thr Ile Lys Ser Val Phe Thr Arg Ser Glu Leu Lys Phe Ser Pro
195 200 205

Gln Trp Ser His His Gly Lys Ile Val Thr Cys Gln Leu Gln Asp Ala
210 215 220

Asp Gly Lys Phe Leu Ser Asn Asp Thr Val Gln Leu Asn Val Lys His
225 230 235 240

Pro Pro Lys Lys Val Thr Thr Val Ile Gln Asn Pro Met Pro Ile Arg
245 250 255

Glu Gly Asp Thr Val Thr Leu Ser Cys Asn Tyr Asn Ser Ser Asn Pro
260 265 270

Ser Val Thr Arg Tyr Glu Trp Lys Pro His Gly Ala Trp Glu Glu Pro
275 280 285

Ser Leu Gly Val Leu Lys Ile Gln Asn Val Gly Trp Asp Asn Thr Thr
290 295 300

Ile Ala Cys Ala Ala Cys Asn Ser Trp Cys Ser Trp Ala Ser Pro Val
305 310 315 320

Ala Leu Asn Val Gln Tyr Ala Pro Arg Asp Val Arg Val Arg Lys Ile
325 330 335

Lys Pro Leu Ser Glu Ile His Ser Gly Asn Ser Val Ser Leu Gln Cys
340 345 350

Asp Phe Ser Ser Ser His Pro Lys Glu Val Gln Phe Phe Trp Glu Lys
355 360 365

Asn Gly Arg Leu Leu Gly Lys Glu Ser Gln Leu Asn Phe Asp Ser Ile
370 375 380

Ser Pro Glu Asp Ala Gly Ser Tyr Ser Cys Trp Val Asn Asn Ser Ile
385 390 395 400

11-88L.ST25.txt

Gly Gln Thr Ala Ser Lys Ala Trp Thr Leu Glu Val Leu Tyr Ala Pro
405 410 415

Arg Arg Leu Arg Val Ser Met Ser Pro Gly Asp Gln Val Met Glu Gly
420 425 430

Lys Ser Ala Thr Leu Thr Cys Glu Ser Asp Ala Asn Pro Pro Val Ser
435 440 445

His Tyr Thr Trp Phe Asp Trp Asn Asn Gln Ser Leu Pro Tyr His Ser
450 455 460

Gln Lys Leu Arg Leu Glu Pro Val Lys Val Gln His Ser Gly Ala Tyr
465 470 475 480

Trp Cys Gln Gly Thr Asn Ser Val Gly Lys Gly Arg Ser Pro Leu Ser
485 490 495

Thr Leu Thr Val Tyr Tyr Ser Pro Glu Thr Ile Gly Arg Arg Val Ala
500 505 510

Val Gly Leu Gly Ser Cys Leu Ala Ile Leu Ile Leu Ala Ile Cys Gly
515 520 525

Leu Lys Leu Gln Arg Arg Trp Lys Arg Thr Gln Ser Gln Gln Gly Leu
530 535 540

Gln Glu Asn Ser Ser Gly Gln Ser Phe Phe Val Arg Asn Lys Lys Val
545 550 555 560

Arg Arg Ala Pro Leu Ser Glu Gly Pro His Ser Leu Gly Cys Tyr Asn
565 570 575

Pro Met Met Glu Asp Gly Ile Ser Tyr Thr Thr Leu Arg Phe Pro Glu
580 585 590

Met Asn Ile Pro Arg Thr Gly Asp Ala Glu Ser Ser Glu Met Gln Arg
595 600 605

Pro Pro Pro Asp Cys Asp Asp Thr Val Thr Tyr Ser Ala Leu His Lys
610 615 620

Arg Gln Val Gly Thr Met Arg Thr Ser Phe Gln Ile Phe Gln Lys Met
625 630 635 640

Arg Gly Phe Ile Thr Gln Ser

11-88L.ST25.txt

645

<210> 28
<211> 1200
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (101)..(880)

<400> 28	ggggtgcaaa gaagagacag cagcgcagg cttggaggtg ctaactccag aggccagcat	60
	cagcaactgg gcacagaaaag gagccgcctg ggcagggacc atg gca cg ^g cca cat	115
	Met Ala Arg Pro His	
	1 5	
	ccc tgg tgg ctg tgc gtt ctg ggg acc ctg gtg ggg ctc tca gct act	163
Pro Trp Trp Leu Cys Val Leu Gly Thr Leu Val Gly Leu Ser Ala Thr		
10 15 20		
	cca gcc ccc aag agc tgc cca gag agg cac tac tgg gct cag gga aag	211
Pro Ala Pro Lys Ser Cys Pro Glu Arg His Tyr Trp Ala Gln Gly Lys		
25 30 35		
	ctg tgc tgc cag atg tgt gag cca gga aca ttc ctc gtg aag gac tgt	259
Leu Cys Cys Gln Met Cys Glu Pro Gly Thr Phe Leu Val Lys Asp Cys		
40 45 50		
	gac cag cat aga aag gct gct cag tgt gat cct tgc ata ccg ggg gtc	307
Asp Gln His Arg Lys Ala Ala Gln Cys Asp Pro Cys Ile Pro Gly Val		
55 60 65		
	tcc ttc tct cct gac cac acc cgg ccc cac tgt gag agc tgt cgg	355
Ser Phe Ser Pro Asp His His Thr Arg Pro His Cys Glu Ser Cys Arg		
70 75 80 85		
	cac tgt aac tct ggt ctt ctc gtt cgc aac tgc acc atc act gcc aat	403
His Cys Asn Ser Gly Leu Leu Val Arg Asn Cys Thr Ile Thr Ala Asn		
90 95 100		
	gct gag tgt gcc tgt cgc aat ggc tgg cag tgc agg gac aag gag tgc	451
Ala Glu Cys Ala Cys Arg Ash Gly Trp Gln Cys Arg Asp Lys Glu Cys		
105 110 115		
	acc gag tgt gat cct ctt cca aac cct tcg ctg acc gct cgg tcg tct	499
Thr Glu Cys Asp Pro Leu Pro Asn Pro Ser Leu Thr Ala Arg Ser Ser		
120 125 130		
	cag gcc ctg agc cca cac cct cag ccc acc cac tta cct tat gtc agt	547
Gln Ala Leu Ser Pro His Pro Gln Pro Thr His Leu Pro Tyr Val Ser		
135 140 145		
	gag atg ctg gag gcc agg aca gct ggg cac atg cag act ctg gct gac	595
Glu Met Leu Glu Ala Arg Thr Ala Gly His Met Gln Thr Leu Ala Asp		
150 155 160 165		
	ttc agg cag ctg cct gcc cgg act ctc tct acc cac tgg cca ccc caa	643
Phe Arg Gln Leu Pro Ala Arg Thr Leu Ser Thr His Trp Pro Pro Gln		
170 175 180		

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aga tcc ctg tgc agc tcc gat ttt att cgc atc ctt gtg atc ttc tct Arg Ser Leu Cys Ser Ser Asp Phe Ile Arg Ile Leu Val Ile Phe Ser	691
185 190 195	
gga atg ttc ctt gtt ttc acc ctg gcc ggg gcc ctg ttc ctc cat caa Gly Met Phe Leu Val Phe Thr Leu Ala Gly Ala Leu Phe Leu His Gln	739
200 205 210	
cga agg aaa tat aga tca aac aaa gga gaa agt cct gtg gag cct gca Arg Arg Lys Tyr Arg Ser Asn Lys Gly Glu Ser Pro Val Glu Pro Ala	787
215 220 225	
gag cct tgt cgt tac agc tgc ccc agg gag gag gag ggc agc acc atc Glu Pro Cys Arg Tyr Ser Cys Pro Arg Glu Glu Glu Gly Ser Thr Ile	835
230 235 240 245	
ccc atc cag gag gat tac cga aaa ccg gag cct gcc tgc tcc ccc Pro Ile Gln Glu Asp Tyr Arg Lys Pro Glu Pro Ala Cys Ser Pro	880
250 255 260	
tgagccagca cctgcggtag ctgcactaca gccctggcct ccaccccccac cccgccgacc atccaaggga gagtgagacc tggcagccac aactgcagtc ccattccttt gtcagggccc	940
tttcctgtgt acacgtgaca gagtgcctt tcgagactgg cagggacgag gacaaatatg gatgaggtgg agagtggaa gcaggagccc agccagctgc gcgccgtgc aggagggcgg	1000
gggctctggt tgtaaggcac acttcctgct gcgaaagacc cacatgctac aagacgggca aaataaaagtg acagatgacc	1060
	1120
	1180
	1200

<210> 29
<211> 260
<212> PRT
<213> Homo sapiens

<400> 29

Met Ala Arg Pro His Pro Trp Trp Leu Cys Val Leu Gly Thr Leu Val
1 5 10 15

Gly Leu Ser Ala Thr Pro Ala Pro Lys Ser Cys Pro Glu Arg His Tyr
20 25 30

Trp Ala Gln Gly Lys Leu Cys Cys Gln Met Cys Glu Pro Gly Thr Phe
35 40 45

Leu Val Lys Asp Cys Asp Gln His Arg Lys Ala Ala Gln Cys Asp Pro
50 55 60

Cys Ile Pro Gly Val Ser Phe Ser Pro Asp His His Thr Arg Pro His
65 70 75 80

Cys Glu Ser Cys Arg His Cys Asn Ser Gly Leu Leu Val Arg Asn Cys
85 90 95

11-88L.ST25.txt

Thr Ile Thr Ala Asn Ala Glu Cys Ala Cys Arg Asn Gly Trp Gln Cys
100 105 110

Arg Asp Lys Glu Cys Thr Glu Cys Asp Pro Leu Pro Asn Pro Ser Leu
115 120 125

Thr Ala Arg Ser Ser Gln Ala Leu Ser Pro His Pro Gln Pro Thr His
130 135 140

Leu Pro Tyr Val Ser Glu Met Leu Glu Ala Arg Thr Ala Gly His Met
145 150 155 160

Gln Thr Leu Ala Asp Phe Arg Gln Leu Pro Ala Arg Thr Leu Ser Thr
165 170 175

His Trp Pro Pro Gln Arg Ser Leu Cys Ser Ser Asp Phe Ile Arg Ile
180 185 190

Leu Val Ile Phe Ser Gly Met Phe Leu Val Phe Thr Leu Ala Gly Ala
195 200 205

Leu Phe Leu His Gln Arg Arg Lys Tyr Arg Ser Asn Lys Gly Glu Ser
210 215 220

Pro Val Glu Pro Ala Glu Pro Cys Arg Tyr Ser Cys Pro Arg Glu Glu
225 230 235 240

Glu Gly Ser Thr Ile Pro Ile Gln Glu Asp Tyr Arg Lys Pro Glu Pro
245 250 255

Ala Cys Ser Pro
260

<210> 30
<211> 2350
<212> DNA
<213> Homo sapiens

<400> 30
ctccctttgg gcaaggacct gagacccttg tgctaagtca agaggctcaa tgggctgcag 60
aagaactaga gaaggaccaa gcaaagccat gatatttcca tggaaatgtc agagcaccca 120
gagggactta tggAACATCT tcaagttgtg ggggtggaca atgctctgtt gtgatttcct 180
ggcacatcat ggaaccgact gctggactta ccattattct gaaaaaccca tgaactggca 240
aaggctaga agattctgcc gagacaatta cacagattt aaaaacaaggc 300
ggaaatttag tatctggaga agactctgcc tttcagtcgt tcttactact ggataggaat 360

11-88L.ST25.txt

ccggaagata ggaggaatat ggacgtgggt gggAACCAAC aaATCTCTCA ctGAAGAACG	420
agagaactgg ggagatggtg agCCCAACAA caAGAAGAAC aaggaggACT gcGTGGAGAT	480
ctatatcaag agaaacaaAG atgcaggCAA atgGAACGAT gacGCCtGCC acaaACTAAA	540
ggcAGCCCTC tgTTACACAG CTTCTGCCA GCCCTGGTCA tgcAGTGGCC atggagaATG	600
tgtAGAAATC atcaATAATT acACCTGCAA CTGTGATGTG gggTACTATG ggCCCCAGTG	660
tcAGTTGTG attCAGTGTG AGCCTTGGA ggCCCCAGAG CTGGTACCA tggACTGTAC	720
tcACTCTTG ggAAACCTCA GCTTCAGCTC ACAGTGTGCC TTCAGTGTCT CTGAAGGAAC	780
aaACTTAACT gggATTGAAG AAACCACCTG TGGACCATT ggAAACTGGT CATCTCCAGA	840
ACCAACCTGT CAAGTGAATC AGTGTGAGCC TCTATCAGCA CCAGATTGG ggATCATGAA	900
CTGTAGCCAT CCCCTGGCCA GCTTCAGCTT TACCTCTGCA TGTACCTTCA TCTGCTCAGA	960
AGGAACtGAG TTAATTGGGA AGAAGAAAAC CATTGTGAA TCACTTGAA TCTGGTCAAA	1020
TCCTAGTCCA ATATGTCAAA AATTGGACAA AAGTTCTCA ATGATTAAGG AGGGTgATTA	1080
taACCCCCTC TTCATTCCAG TGGCAGTCAT GGTtACTGCA TTCTCTGGGT TGGCATTAT	1140
CATTGGCTG GCAAGGAGAT TAAAAAAAGG CAAGAAATCC AAGAGAAGTA TGAATGACCC	1200
ATATTAAATC GCCCTTGGTG AAAGAAAATT CTTGGAATAC TAAAAATCAT GAGATCCTT	1260
AAATCCTTCC ATGAAACGTT TTGTGTGGTG GCACCTCCTA CGTCAAACAT GAAGTGTGTT	1320
TCCttCAGTG CATCTGGAA GATTCTACC TGACCAACAG TTCCTTCAGC TTCCATTTCG	1380
CCCCTCATTt ATCCCTCAAC CCCCAGCCCA CAGGTGTTA TACAGCTCAG CTTTTGTCT	1440
TTTCTGAGGA GAAACAAATA AGACCATAAA GGGAAAGGAT TCACTTGAA TATAAAGATG	1500
GCTGACTTTG CTCTTCTTG ACTCTTGTtT TCAgTTCAA TTCAGTGTG TACTTGATGA	1560
CAGACACTTC TAAATGAAGT GCAAATTGA TACATATGTG AATATGGACT CAGTTTCTT	1620
GCAgATCAAa TTTCACGTG TCTTCTGTAT ACTGTGGAGG TACACTCTTA TAGAAAGTTC	1680
AAAAGTCTA CGCTCTCCTT TCTTCTCAAC TCCAGTGAAG TAATGGGTC CTGCTCAAGT	1740
TGAAAGAGTC CTATTTGCAC TGTAGCCTG CCGTCTGTGA ATTGGACCAT CCTATTAAAC	1800
TGGCTTCAGC CTCCCCACCT TCTTCAGCCA CCTCTCTTT TCAGTTGGCT GACTTCCACa	1860
CCTAGCATCT CATGAGTGCC AAGCAAAAGG AGAGAAGAGA GAAATAGCCT GCGCTGTTT	1920
TTAGTTGGG GGTTTGCTG TTTCTTTA TGAGACCCAT TCCTATTCT TATAGTCAAT	1980
GTTTCTTTA TCACGATATT ATTAGTAAGA AAACATCACT GAAATGCTAG CTGCAAGTGA	2040
CATCTCTTG ATGTCAATG GAAGAGTTAA AACAGGTGGA GAAATTCCCTT GATTCAACAT	2100
GAAATGCTCT CTTTCCCT GCCCCAGAC CTTTATCCG ACTTACCTAG ATTCTACATA	2160
TTCTTAAAT TTCATCTCAG GCCTCCCTCA ACCCCACCAc TTCTTTATA ACTAGTCCTT	2220

11-88L.ST25.txt

tactaatcca	acccatgatg	agctcctctt	cctggcttct	tactgaaagg	ttaccctgt	a	2280
acatgcattt	ttgcatttga	ataaagcctg	cttttaagt	gttaaaaaaaa	aaaaaaaaaa	a	2340
aaaaaaaaaa							2350

<210> 31
<211> 1354
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (116)..(1198)

<400> 31	ccagcctctg	ccaggttcgg	tccgccatcc	tcgtcccg	ctccgcccgc	ccctgccccg	60
cgcccaggga	tcctccagct	ccttcgccc	gcccctccg	ttcgctccgg	acacc	atg	118
						Met	
						1	
gac aag ttt tgg tgg cac gca gcc tgg gga ctc tgc ctc	gtg ccg ctg	Asp Lys Phe Trp Trp His Ala Ala Trp Gly Leu Cys Leu Val Pro Leu	166				
5	10	15					
agc ctg gcg cag atc gat ttg aat ata acc tgc cgc ttt gca ggt gta	Ser Leu Ala Gln Ile Asp Leu Asn Ile Thr Cys Arg Phe Ala Gly Val	214					
20	25	30					
ttc cac gtg gag aaa aat ggt cgc tac agc atc tct cgg acg gag gcc	Phe His Val Glu Lys Asn Gly Arg Tyr Ser Ile Ser Arg Thr Glu Ala	262					
35	40	45					
gct gac ctc tgc aag gct ttc aat agc acc ttg ccc aca atg gcc cag	Ala Asp Leu Cys Lys Ala Phe Asn Ser Thr Leu Pro Thr Met Ala Gln	310					
50	55	60	65				
atg gag aaa gct ctg agc atc gga ttt gag acc tgc agg tat ggg ttc	Met Glu Lys Ala Leu Ser Ile Gly Phe Glu Thr Cys Arg Tyr Gly Phe	358					
70	75	80					
ata gaa ggg cat gtg gtg att ccc cgg atc cac ccc aac tcc atc tgt	Ile Glu Gly His Val Val Ile Pro Arg Ile His Pro Asn Ser Ile Cys	406					
85	90	95					
gca gca aac aac aca ggg gtg tac atc ctc aca tac aac acc tcc cag	Ala Ala Asn Asn Thr Gly Val Tyr Ile Leu Thr Tyr Asn Thr Ser Gln	454					
100	105	110					
tat gac aca tat tgc ttc aat gct tca gct cca cct gaa gaa gat tgt	Tyr Asp Thr Tyr Cys Phe Asn Ala Ser Ala Pro Pro Glu Glu Asp Cys	502					
115	120	125					
aca tca gtc aca gac ctg ccc aat gcc ttt gat gga cca att acc ata	Thr Ser Val Thr Asp Leu Pro Asn Ala Phe Asp Gly Pro Ile Thr Ile	550					
130	135	140	145				
act att gtt aac cgt gat ggc acc cgc tat gtc cag aaa gga gaa tac	Thr Ile Val Asn Arg Asp Gly Thr Arg Tyr Val Gln Lys Gly Glu Tyr	598					
150	155	160					

11-88L.ST25.txt

aga acg aat cct gaa gac atc tac ccc agc aac cct act gat gat gac Arg Thr Asn Pro Glu Asp Ile Tyr Pro Ser Asn Pro Thr Asp Asp Asp 165 170 175	646
gtg agc agc ggc tcc tcc agt gaa agg agc agc act tca gga ggt tac Val Ser Ser Gly Ser Ser Glu Arg Ser Ser Thr Ser Gly Gly Tyr 180 185 190	694
atc ttt tac acc ttt tct act gta cac ccc atc cca gac gaa gac agt Ile Phe Tyr Thr Phe Ser Thr Val His Pro Ile Pro Asp Glu Asp Ser 195 200 205	742
ccc tgg atc acc gac agc aca gac aga atc cct gct acc aga gac caa Pro Trp Ile Thr Asp Ser Thr Asp Arg Ile Pro Ala Thr Arg Asp Gln 210 215 220 225	790
gac aca ttc cac ccc agt ggg ggg tcc cat acc act cat gaa tct gaa Asp Thr Phe His Pro Ser Gly Gly Ser His Thr Thr His Glu Ser Glu 230 235 240	838
tca gat gga cac tca cat ggg agt caa gaa ggt gga gca aac aca acc Ser Asp Gly His Ser His Gly Ser Gln Glu Gly Gly Ala Asn Thr Thr 245 250 255	886
tct ggt cct ata agg aca ccc caa att cca gaa tgg ctg atc atc ttg Ser Gly Pro Ile Arg Thr Pro Gln Ile Pro Glu Trp Leu Ile Ile Leu 260 265 270	934
gca tcc ctc ttg gcc ttg gct ttg att ctt gca gtt tgc att gca gtc Ala Ser Leu Leu Ala Leu Ala Leu Ile Leu Ala Val Cys Ile Ala Val 275 280 285	982
aac agt cga aga agg tgt ggg cag aag aaa aag cta gtg atc aac agt Asn Ser Arg Arg Arg Cys Gly Gln Lys Lys Lys Leu Val Ile Asn Ser 290 295 300 305	1030
ggc aat gga gct gtg gag gac aga aag cca agt gga ctc aac gga gag Gly Asn Gly Ala Val Glu Asp Arg Lys Pro Ser Gly Leu Asn Gly Glu 310 315 320	1078
gcc agc aag tct cag gaa atg gtg cat ttg gtg aac aag gag tcg tca Ala Ser Lys Ser Gln Glu Met Val His Leu Val Asn Lys Glu Ser Ser 325 330 335	1126
gaa act cca gac cag ttt atg aca gct gat gag aca agg aac ctg cag Glu Thr Pro Asp Gln Phe Met Thr Ala Asp Glu Thr Arg Asn Leu Gln 340 345 350	1174
aat gtg gac atg aag att ggg gtg taacacctac accattatct tggaaaagaaa Asn Val Asp Met Lys Ile Gly Val 355 360	1228
caaccgttgt aaacataacc attacaggga gctggacac ttaacagatg caatgtgcta ctgattgttt cattgcgaat ctttttagc ataaaatttt ctacttttt tgtaaaaaaa	1288
aaaaaaaa	1348
	1354

<210> 32
<211> 361
<212> PRT

11-88L.ST25.txt

<213> Homo sapiens

<400> 32

Met Asp Lys Phe Trp Trp His Ala Ala Trp Gly Leu Cys Leu Val Pro
1 5 10 15

Leu Ser Leu Ala Gln Ile Asp Leu Asn Ile Thr Cys Arg Phe Ala Gly
20 25 30

Val Phe His Val Glu Lys Asn Gly Arg Tyr Ser Ile Ser Arg Thr Glu
35 40 45

Ala Ala Asp Leu Cys Lys Ala Phe Asn Ser Thr Leu Pro Thr Met Ala
50 55 60

Gln Met Glu Lys Ala Leu Ser Ile Gly Phe Glu Thr Cys Arg Tyr Gly
65 70 75 80

Phe Ile Glu Gly His Val Val Ile Pro Arg Ile His Pro Asn Ser Ile
85 90 95

Cys Ala Ala Asn Asn Thr Gly Val Tyr Ile Leu Thr Tyr Asn Thr Ser
100 105 110

Gln Tyr Asp Thr Tyr Cys Phe Asn Ala Ser Ala Pro Pro Glu Glu Asp
115 120 125

Cys Thr Ser Val Thr Asp Leu Pro Asn Ala Phe Asp Gly Pro Ile Thr
130 135 140

Ile Thr Ile Val Asn Arg Asp Gly Thr Arg Tyr Val Gln Lys Gly Glu
145 150 155 160

Tyr Arg Thr Asn Pro Glu Asp Ile Tyr Pro Ser Asn Pro Thr Asp Asp
165 170 175

Asp Val Ser Ser Gly Ser Ser Glu Arg Ser Ser Thr Ser Gly Gly
180 185 190

Tyr Ile Phe Tyr Thr Phe Ser Thr Val His Pro Ile Pro Asp Glu Asp
195 200 205

Ser Pro Trp Ile Thr Asp Ser Thr Asp Arg Ile Pro Ala Thr Arg Asp
210 215 220

Gln Asp Thr Phe His Pro Ser Gly Gly Ser His Thr Thr His Glu Ser
225 230 235 240

11-88L.ST25.txt

Glu Ser Asp Gly His Ser His Gly Ser Gln Glu Gly Gly Ala Asn Thr
245 250 255

Thr Ser Gly Pro Ile Arg Thr Pro Gln Ile Pro Glu Trp Leu Ile Ile
260 265 270

Leu Ala Ser Leu Leu Ala Leu Ala Leu Ile Leu Ala Val Cys Ile Ala
275 280 285

Val Asn Ser Arg Arg Arg Cys Gly Gln Lys Lys Lys Leu Val Ile Asn
290 295 300

Ser Gly Asn Gly Ala Val Glu Asp Arg Lys Pro Ser Gly Leu Asn Gly
305 310 315 320

Glu Ala Ser Lys Ser Gln Glu Met Val His Leu Val Asn Lys Glu Ser
325 330 335

Ser Glu Thr Pro Asp Gln Phe Met Thr Ala Asp Glu Thr Arg Asn Leu
340 345 350

Gln Asn Val Asp Met Lys Ile Gly Val
355 360

<210> 33
<211> 2308
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (116)..(1594)

<400> 33
ccagcctctg ccaggttcgg tccgccatcc tcgtcccgta ctccgcggc ccctgccccg 60

cgcgcaggaa tcctccagct ctttcgccc gcgcgcctccg ttgcgtccgg acacc atg 118
Met 1

gac aag ttt tgg tgg cac gca gcc tgg gga ctc tgc ctc gtg ccg ctg 166
Asp Lys Phe Trp Trp His Ala Ala Trp Gly Leu Cys Leu Val Pro Leu
5 10 15

agc ctg gcg cag atc gat ttg aat ata acc tgc cgc ttt gca ggt gta 214
Ser Leu Ala Gln Ile Asp Leu Asn Ile Thr Cys Arg Phe Ala Gly Val
20 25 30

ttc cac gtg gag aaa aat ggt cgc tac agc atc tct cgg acg gag gcc 262
Phe His Val Glu Lys Asn Gly Arg Tyr Ser Ile Ser Arg Thr Glu Ala
35 40 45

gct gac ctc tgc aag gct ttc aat agc acc ttg ccc aca atg gcc cag 310

11-88L.ST25.txt

Ala Asp Leu Cys Lys Ala Phe Asn Ser Thr Leu Pro Thr Met Ala Gln	
50 55 60 65	
atg gag aaa gct ctg agc atc gga ttt gag acc tgc agg tat ggg ttc	358
Met Glu Lys Ala Leu Ser Ile Gly Phe Glu Thr Cys Arg Tyr Gly Phe	
70 75 80	
ata gaa ggg cat gtg gtg att ccc cggtt acc tac ccc aac tcc atc tgt	406
Ile Glu Gly His Val Val Ile Pro Arg Ile His Pro Asn Ser Ile Cys	
85 90 95	
gca gca aac aac aca ggg gtg tac atc ctc aca tac aac acc tcc cag	454
Ala Ala Asn Asn Thr Gly Val Tyr Ile Leu Thr Tyr Asn Thr Ser Gln	
100 105 110	
tat gac aca tat tgc ttc aat gct tca gct cca cct gaa gaa gat tgt	502
Tyr Asp Thr Tyr Cys Phe Asn Ala Ser Ala Pro Pro Glu Glu Asp Cys	
115 120 125	
aca tca gtc aca gac ctg ccc aat gcc ttt gat gga cca att acc ata	550
Thr Ser Val Thr Asp Leu Pro Asn Ala Phe Asp Gly Pro Ile Thr Ile	
130 135 140 145	
act att gtt aac cgt gat ggc acc cgc tat gtc cag aaa gga gaa tac	598
Thr Ile Val Asn Arg Asp Gly Thr Arg Tyr Val Gln Lys Gly Glu Tyr	
150 155 160	
aga acg aat cct gaa gac atc tac ccc agc aac cct act gat gat gac	646
Arg Thr Asn Pro Glu Asp Ile Tyr Pro Ser Asn Pro Thr Asp Asp Asp	
165 170 175	
gtg agc agc ggc tcc tcc agt gaa agg agc agc act tca gga ggt tac	694
Val Ser Ser Gly Ser Ser Glu Arg Ser Ser Thr Ser Gly Gly Tyr	
180 185 190	
atc ttt tac acc ttt tct act gta cac ccc atc cca gac gaa gac agt	742
Ile Phe Tyr Thr Phe Ser Thr Val His Pro Ile Pro Asp Glu Asp Ser	
195 200 205	
ccc tgg atc acc gac agc aca gac aga atc cct cgt acc aat atg gac	790
Pro Trp Ile Thr Asp Ser Thr Asp Arg Ile Pro Arg Thr Asn Met Asp	
210 215 220 225	
tcc agt cat agt aca acg ctt cag cct act gca aat cca aac aca ggt	838
Ser Ser His Ser Thr Thr Leu Gln Pro Thr Ala Asn Pro Asn Thr Gly	
230 235 240	
ttg gtg gaa gat ttg gac agg aca gga cct ctt tca atg aca acg cag	886
Leu Val Glu Asp Leu Asp Arg Thr Gly Pro Leu Ser Met Thr Thr Gln	
245 250 255	
cag agt aat tct cag agc ttc tct aca tca cat gaa ggc ttg gaa gaa	934
Gln Ser Asn Ser Gln Ser Phe Ser Thr Ser His Glu Gly Leu Glu Glu	
260 265 270	
gat aaa gac cat cca aca act tct act ctg aca tca agc aat agg aat	982
Asp Lys Asp His Pro Thr Thr Ser Thr Leu Thr Ser Ser Asn Arg Asn	
275 280 285	
gat gtc aca ggt gga aga aga gac cca aat cat tct gaa ggc tca act	1030
Asp Val Thr Gly Gly Arg Arg Asp Pro Asn His Ser Glu Gly Ser Thr	
290 295 300 305	

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cat tta ctg gaa ggt tat acc tct cat tac cca cac acg aag gaa agc His Leu Leu Glu Gly Tyr Thr Ser His Tyr Pro His Thr Lys Glu Ser 310 315 320	1078
agg acc ttc atc cca gtg acc tca gct aag act ggg tcc ttt gga gtt Arg Thr Phe Ile Pro Val Thr Ser Ala Lys Thr Gly Ser Phe Gly Val 325 330 335	1126
act gca gtt act gtt gga gat tcc aac tct aat gtc aat cgt tcc tta Thr Ala Val Thr Val Gly Asp Ser Asn Ser Asn Val Asn Arg Ser Leu 340 345 350	1174
tca gga gac caa gac aca ttc cac ccc agt ggg ggg tcc cat acc act Ser Gly Asp Gln Asp Thr Phe His Pro Ser Gly Gly Ser His Thr Thr 355 360 365	1222
cat gga tct gaa tca gat gga cac tca cat ggg agt caa gaa ggt gga His Gly Ser Glu Ser Asp Gly His Ser His Gly Ser Gln Glu Gly Gly 370 375 380 385	1270
gca aac aca acc tct ggt cct ata agg aca ccc caa att cca gaa tgg Ala Asn Thr Thr Ser Gly Pro Ile Arg Thr Pro Gln Ile Pro Glu Trp 390 395 400	1318
ctg atc atc ttg gca tcc ctc ttg gcc ttg gct ttg att ctt gca gtt Leu Ile Ile Leu Ala Ser Leu Leu Ala Leu Ala Leu Ile Leu Ala Val 405 410 415	1366
tgc att gca gtc aac agt cga aga agg tgt ggg cag aag aaa aag cta Cys Ile Ala Val Asn Ser Arg Arg Arg Cys Gly Gln Lys Lys Lys Leu 420 425 430	1414
gtg atc aac agt ggc aat gga gct gtg gag gac aga aag cca agt gga Val Ile Asn Ser Gly Asn Gly Ala Val Glu Asp Arg Lys Pro Ser Gly 435 440 445	1462
ctc aac gga gag gcc agc aag tct cag gaa atg gtg cat ttg gtg aac Leu Asn Gly Glu Ala Ser Lys Ser Gln Glu Met Val His Leu Val Asn 450 455 460 465	1510
aag gag tcg tca gaa act cca gac cag ttt atg aca gct gat gag aca Lys Glu Ser Ser Glu Thr Pro Asp Gln Phe Met Thr Ala Asp Glu Thr 470 475 480	1558
agg aac ctg cag aat gtg gac atg aag att ggg gtg taacacctac Arg Asn Leu Gln Asn Val Asp Met Lys Ile Gly Val 485 490	1604
accattatct tggaaagaaa caacgttgg aacataacca ttacagggga gctgggacac	1664
ttaacagatg caatgtgcta ctgattgttt catttcgaat ctataatgc ataaaatttt	1724
ctacttttt tgtttttgt gttttttct tttaaagttagtgc gtccaatttg taaaaacagc	1784
attgcattttct gaaatttaggg cccaaatataat aatcagcaag aattttgatc gtttcagttc	1844
cccacttggga ggcctttcat ccctcggttg tgctatggat ggcttctaacc aaaaacctac	1904
cacatagtta ttccctgatcg ccaaccttgc cccccaccag ctaaggacat ttccagggtt	1964
aatagggcct ggtcctggga ggaaatttga atgggtcatt ttgcccttcc attagcctaa	2024
tccctggca ttgctttcca ctgaggttgg ggggtgggt gtactagtta cacatcttca	2084

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acagacccccc tctagaaatt tttcagatgc ttctggaga cacccaaagg gtaagtctat 2144
ttatctgttag taaactattt atctgtgttt ttgaaatatt aaaccctgga tcagtccttt 2204
tattcagtat aattttttaa agttactttg tcagaggcac aaaaagggtt taaactgatt 2264
cataataaat atctgtacct tcattcgaaaa aaaaaaaaaa aaaa 2308

<210> 34
<211> 493
<212> PRT
<213> Homo sapiens

<400> 34

Met Asp Lys Phe Trp Trp His Ala Ala Trp Gly Leu Cys Leu Val Pro
1 5 10 15

Leu Ser Leu Ala Gln Ile Asp Leu Asn Ile Thr Cys Arg Phe Ala Gly
20 25 30

Val Phe His Val Glu Lys Asn Gly Arg Tyr Ser Ile Ser Arg Thr Glu
35 40 45

Ala Ala Asp Leu Cys Lys Ala Phe Asn Ser Thr Leu Pro Thr Met Ala
50 55 60

Gln Met Glu Lys Ala Leu Ser Ile Gly Phe Glu Thr Cys Arg Tyr Gly
65 70 75 80

Phe Ile Glu Gly His Val Val Ile Pro Arg Ile His Pro Asn Ser Ile
85 90 95

Cys Ala Ala Asn Asn Thr Gly Val Tyr Ile Leu Thr Tyr Asn Thr Ser
100 105 110

Gln Tyr Asp Thr Tyr Cys Phe Asn Ala Ser Ala Pro Pro Glu Glu Asp
115 120 125

Cys Thr Ser Val Thr Asp Leu Pro Asn Ala Phe Asp Gly Pro Ile Thr
130 135 140

Ile Thr Ile Val Asn Arg Asp Gly Thr Arg Tyr Val Gln Lys Gly Glu
145 150 155 160

Tyr Arg Thr Asn Pro Glu Asp Ile Tyr Pro Ser Asn Pro Thr Asp Asp
165 170 175

Asp Val Ser Ser Gly Ser Ser Ser Glu Arg Ser Ser Thr Ser Gly Gly
180 185 190

11-88L.ST25.txt

Tyr Ile Phe Tyr Thr Phe Ser Thr Val His Pro Ile Pro Asp Glu Asp
195 200 205

Ser Pro Trp Ile Thr Asp Ser Thr Asp Arg Ile Pro Arg Thr Asn Met
210 215 220

Asp Ser Ser His Ser Thr Thr Leu Gln Pro Thr Ala Asn Pro Asn Thr
225 230 235 240

Gly Leu Val Glu Asp Leu Asp Arg Thr Gly Pro Leu Ser Met Thr Thr
245 250 255

Gln Gln Ser Asn Ser Gln Ser Phe Ser Thr Ser His Glu Gly Leu Glu
260 265 270

Glu Asp Lys Asp His Pro Thr Thr Ser Thr Leu Thr Ser Ser Asn Arg
275 280 285

Asn Asp Val Thr Gly Gly Arg Arg Asp Pro Asn His Ser Glu Gly Ser
290 295 300

Thr His Leu Leu Glu Gly Tyr Thr Ser His Tyr Pro His Thr Lys Glu
305 310 315 320

Ser Arg Thr Phe Ile Pro Val Thr Ser Ala Lys Thr Gly Ser Phe Gly
325 330 335

Val Thr Ala Val Thr Val Gly Asp Ser Asn Ser Asn Val Asn Arg Ser
340 345 350

Leu Ser Gly Asp Gln Asp Thr Phe His Pro Ser Gly Gly Ser His Thr
355 360 365

Thr His Gly Ser Glu Ser Asp Gly His Ser His Gly Ser Gln Glu Gly
370 375 380

Gly Ala Asn Thr Thr Ser Gly Pro Ile Arg Thr Pro Gln Ile Pro Glu
385 390 395 400

Trp Leu Ile Ile Leu Ala Ser Leu Leu Ala Leu Ala Leu Ile Leu Ala
405 410 415

Val Cys Ile Ala Val Asn Ser Arg Arg Arg Cys Gly Gln Lys Lys Lys
420 425 430

Leu Val Ile Asn Ser Gly Asn Gly Ala Val Glu Asp Arg Lys Pro Ser
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435

440

445

Gly Leu Asn Gly Glu Ala Ser Lys Ser Gln Glu Met Val His Leu Val
 450 455 460

Asn Lys Glu Ser Ser Glu Thr Pro Asp Gln Phe Met Thr Ala Asp Glu
 465 470 475 480

Thr Arg Asn Leu Gln Asn Val Asp Met Lys Ile Gly Val
 485 490

<210> 35
 <211> 1452
 <212> DNA
 <213> Homo sapiens

<220>
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<400> 35
 ctcaaggata atcactaaat tctgccgaaa ggactgagga acggtgccctg gaaaaggcca 60

agaatatcac ggc atg ggc atg agt agc ttg aaa ctg ctg aag tat gtc 109
 Met Gly Met Ser Ser Leu Lys Leu Leu Lys Tyr Val
 1 5 10

ctg ttt ttc ttc aac ttg ctc ttt tgg atc tgt ggc tgc tgc att ttg 157
 Leu Phe Phe Asn Leu Leu Phe Trp Ile Cys Gly Cys Cys Ile Leu
 15 20 25

ggc ttt ggg atc tac ctg ctg atc cac aac aac ttc gga gtg ctc ttc 205
 Gly Phe Gly Ile Tyr Leu Leu Ile His Asn Asn Phe Gly Val Leu Phe
 30 35 40

cat aac ctc ccc tcc ctc acg ctg ggc aat gtg ttt gtc atc gtg ggc 253
 His Asn Leu Pro Ser Leu Thr Leu Gly Asn Val Phe Val Ile Val Gly
 45 50 55 60

tct att atc atg gta gtt gcc ttc ctg ggc tgc atg ggc tct atc aag 301
 Ser Ile Ile Met Val Val Ala Phe Leu Gly Cys Met Gly Ser Ile Lys
 65 70 75

gaa aac aag tgt ctg ctt atg tcg ttc ttc atc ctg ctg ctg att atc 349
 Glu Asn Lys Cys Leu Leu Met Ser Phe Phe Ile Leu Leu Leu Ile Ile
 80 85 90

ctc ctt gct gag gtg acc ttg gcc atc ctg ctc ttt gta tat gaa cag 397
 Leu Leu Ala Glu Val Thr Leu Ala Ile Leu Leu Phe Val Tyr Glu Gln
 95 100 105

aag ctg aat gag tat gtg gct aag ggt ctg acc gac agc atc cac cgt 445
 Lys Leu Asn Glu Tyr Val Ala Lys Gly Leu Thr Asp Ser Ile His Arg
 110 115 120

tac cac tca gac aat agc acc aag gca gcg tgg gac tcc atc cag tca 493
 Tyr His Ser Asp Asn Ser Thr Lys Ala Ala Trp Asp Ser Ile Gln Ser
 125 130 135 140

11-88L.ST25.txt

ttt ctg cag tgt tgt ggt ata aat ggc acg agt gat tgg acc agt ggc Phe Leu Gln Cys Cys Gly Ile Asn Gly Thr Ser Asp Trp Thr Ser Gly 145 150 155	541
cca cca gca tct tgc ccc tca gat cga aaa gtg gag ggt tgc tat gcg Pro Pro Ala Ser Cys Pro Ser Asp Arg Lys Val Glu Gly Cys Tyr Ala 160 165 170	589
aaa gca aga ctg tgg ttt cat tcc aat ttc ctg tat atc gga atc atc Lys Ala Arg Leu Trp Phe His Ser Asn Phe Leu Tyr Ile Gly Ile Ile 175 180 185	637
acc atc tgt gta tgt gtg att gag gtg ttg ggg atg tcc ttt gca ctg Thr Ile Cys Val Cys Val Ile Glu Val Leu Gly Met Ser Phe Ala Leu 190 195 200	685
acc ctg aac tgc cag att gac aaa acc agc cag acc ata ggg cta Thr Leu Asn Cys Gln Ile Asp Lys Thr Ser Gln Thr Ile Gly Leu 205 210 215	730
tgatctgcag tagttctgtg gtgaagagac ttgtttcatc tccggaaatg caaaaaccatt tatagcatga agccctacat gatcaactgca ggatgatcct cctcccatcc tttccctttt taggtccctg tcttatacaa ccagagaagt gggtgttggc caggcacatc ccatctcagg cagcaagaca atctttcact cactgacggc agcagccatg tctctcaaag tggtaaact aatatctgag catcttttag acaagagagg caaagacaaa ctggatttaa tggcccaaca tcaaagggtg aacccaggat atgaattttt gcatcttccc attgtcgaat tagtctccag cctctaaata atgcccagtc ttctccccaa agtcaagcaa gagactagtt gaagggagtt ctggggccag gctcaactgga ccattgtcac aaccctctgt ttctcttga ctaagtgcc tggctacagg aattacacag ttctcttct ccaaaggca agatctcatt tcaatttctt tattagaggg ctttattgat gtgttctaag tctttccaga aaaaaactat ccagtgattt atatcctgat ttcaaccagt cacttagctg ataatcacag taagaagact tctggtatta tctctatc agataagatt ttgttaatgt actatttac tcttcaataa ataaaacagt tt	790 850 910 970 1030 1090 1150 1210 1270 1330 1390 1450 1452

<210> 36
<211> 219
<212> PRT
<213> Homo sapiens
<400> 36

Met Gly Met Ser Ser Leu Lys Leu Leu Lys Tyr Val Leu Phe Phe Phe
1 5 10 15

Asn Leu Leu Phe Trp Ile Cys Gly Cys Cys Ile Leu Gly Phe Gly Ile
20 25 30

11-88L.ST25.txt

Tyr Leu Leu Ile His Asn Asn Phe Gly Val Leu Phe His Asn Leu Pro
35 40 45

Ser Leu Thr Leu Gly Asn Val Phe Val Ile Val Gly Ser Ile Ile Met
50 55 60

Val Val Ala Phe Leu Gly Cys Met Gly Ser Ile Lys Glu Asn Lys Cys
65 70 75 80

Leu Leu Met Ser Phe Phe Ile Leu Leu Ile Ile Leu Leu Ala Glu
85 90 95

Val Thr Leu Ala Ile Leu Leu Phe Val Tyr Glu Gln Lys Leu Asn Glu
100 105 110

Tyr Val Ala Lys Gly Leu Thr Asp Ser Ile His Arg Tyr His Ser Asp
115 120 125

Asn Ser Thr Lys Ala Ala Trp Asp Ser Ile Gln Ser Phe Leu Gln Cys
130 135 140

Cys Gly Ile Asn Gly Thr Ser Asp Trp Thr Ser Gly Pro Pro Ala Ser
145 150 155 160

Cys Pro Ser Asp Arg Lys Val Glu Gly Cys Tyr Ala Lys Ala Arg Leu
165 170 175

Trp Phe His Ser Asn Phe Leu Tyr Ile Gly Ile Ile Thr Ile Cys Val
180 185 190

Cys Val Ile Glu Val Leu Gly Met Ser Phe Ala Leu Thr Leu Asn Cys
195 200 205

Gln Ile Asp Lys Thr Ser Gln Thr Ile Gly Leu
210 215

<210> 37

<211> 12

<212> DNA

<213> Artificial

<220>

<223> oligonucleotide primer

<400> 37

cttttagagca ca

12

<210> 38

<211> 9

<212> PRT

11-88L.ST25.txt

<213> Artificial

<220>

<223> Synthetic peptide

<220>

<221> VARIANT

<222> (1)..(9)

<223> Xaa at positions 1 and 4 can be any amino acid

<400> 38

Xaa Pro Pro Xaa Ala Ser Ala Leu Pro
1 5

<210> 39

<211> 240

<212> PRT

<213> Homo sapiens

<400> 39

Met Ala Gly Pro Pro Arg Leu Leu Leu Pro Leu Leu Leu Ala Leu
1 5 10 15

Ala Arg Gly Leu Pro Gly Ala Leu Ala Ala Gln Glu Val Gln Gln Ser
20 25 30

Pro His Cys Thr Thr Val Pro Val Gly Ala Ser Val Asn Ile Thr Cys
35 40 45

Ser Thr Ser Gly Gly Leu Arg Gly Ile Tyr Leu Arg Gln Leu Gly Pro
50 55 60

Gln Pro Gln Asp Ile Ile Tyr Tyr Glu Asp Gly Val Val Pro Thr Thr
65 70 75 80

Asp Arg Arg Phe Glu Gly Arg Ile Asp Phe Ser Gly Ser Gln Asp Asn
85 90 95

Leu Thr Ile Thr Met His Arg Leu Gln Leu Ser Asp Thr Gly Thr Tyr
100 105 110

Thr Cys Gln Ala Ile Thr Glu Val Asn Val Tyr Gly Ser Gly Thr Leu
115 120 125

Val Leu Val Thr Glu Glu Gln Ser Gln Gly Trp His Arg Cys Ser Asp
130 135 140

Ala Pro Pro Arg Ala Ser Ala Leu Pro Ala Pro Pro Thr Gly Ser Ala
145 150 155 160

11-88L.ST25.txt

Leu Pro Asp Pro Gln Thr Ala Ser Ala Leu Pro Asp Pro Pro Ala Ala
165 170 175

Ser Ala Leu Pro Ala Ala Leu Ala Val Ile Ser Phe Leu Leu Gly Leu
180 185 190

Gly Leu Gly Val Ala Cys Val Leu Ala Arg Thr Gln Ile Lys Lys Leu
195 200 205

Cys Ser Trp Arg Asp Lys Asn Ser Ala Ala Cys Val Val Tyr Glu Asp
210 215 220

Met Ser His Ser Arg Cys Asn Thr Leu Ser Ser Pro Asn Gln Tyr Gln
225 230 235 240

<210> 40

<211> 311

<212> PRT

<213> Homo sapiens

<400> 40

Met Ser Gln Asn Val Cys Pro Arg Asn Leu Trp Leu Leu Gln Pro Leu
1 5 10 15

Thr Val Leu Leu Leu Ala Ser Ala Asp Ser Gln Ala Ala Ala Pro
20 25 30

Pro Lys Ala Val Leu Lys Leu Glu Pro Pro Trp Ile Asn Val Leu Gln
35 40 45

Glu Asp Ser Val Thr Leu Thr Cys Gln Gly Ala Arg Ser Pro Glu Ser
50 55 60

Asp Ser Ile Gln Trp Phe His Asn Gly Asn Leu Ile Pro Thr His Thr
65 70 75 80

Gln Pro Ser Tyr Arg Phe Lys Ala Asn Asn Asn Asp Ser Gly Glu Tyr
85 90 95

Thr Cys Gln Thr Gly Gln Thr Ser Leu Ser Asp Pro Val His Leu Thr
100 105 110

Val Leu Ser Glu Trp Leu Val Leu Gln Thr Pro His Leu Glu Phe Gln
115 120 125

Glu Gly Glu Thr Ile Met Leu Arg Cys His Ser Trp Lys Asp Lys Pro
130 135 140

11-88L.ST25.txt

Leu Val Lys Val Thr Phe Phe Gln Asn Gly Lys Ser Gln Lys Phe Ser
145 150 155 160

Arg Leu Asp Pro Thr Phe Ser Ile Pro Gln Ala Asn His Ser His Ser
165 170 175

Gly Asp Tyr His Cys Thr Gly Asn Ile Gly Tyr Thr Leu Phe Ser Ser
180 185 190

Lys Pro Val Thr Ile Thr Val Gln Val Pro Ser Met Gly Ser Ser Ser
195 200 205

Pro Met Gly Ile Ile Val Ala Val Val Ile Ala Thr Ala Val Ala Ala
210 215 220

Ile Val Ala Ala Val Val Ala Leu Ile Tyr Cys Arg Lys Lys Arg Ile
225 230 235 240

Ser Ala Asn Ser Thr Asp Pro Val Lys Ala Ala Gln Phe Glu Pro Pro
245 250 255

Gly Arg Gln Met Ile Ala Ile Arg Lys Arg Gln Leu Glu Glu Thr Asn
260 265 270

Asn Asp Tyr Glu Thr Ala Asp Gly Gly Tyr Met Thr Leu Asn Pro Arg
275 280 285

Ala Pro Thr Asp Asp Asp Lys Asn Ile Tyr Leu Thr Leu Pro Pro Asn
290 295 300

Asp His Val Asn Ser Asn Asn
305 310

<210> 41
<211> 385
<212> PRT
<213> Homo sapiens

<400> 41

Met Gly Cys Arg Arg Thr Arg Glu Gly Pro Ser Lys Ala Met Ile Phe
1 5 10 15

Pro Trp Lys Cys Gln Ser Thr Gln Arg Asp Leu Trp Asn Ile Phe Lys
20 25 30

Leu Trp Gly Trp Thr Met Leu Cys Cys Asp Phe Leu Ala His His Gly
35 40 45

11-88L.ST25.txt

Thr Asp Cys Trp Thr Tyr His Tyr Ser Glu Lys Pro Met Asn Trp Gln
50 55 60

Arg Ala Arg Arg Phe Cys Arg Asp Asn Tyr Thr Asp Leu Val Ala Ile
65 70 75 80

Gln Asn Lys Ala Glu Ile Glu Tyr Leu Glu Lys Thr Leu Pro Phe Ser
85 90 95

Arg Ser Tyr Tyr Trp Ile Gly Ile Arg Lys Ile Gly Gly Ile Trp Thr
100 105 110

Trp Val Gly Thr Asn Lys Ser Leu Thr Glu Glu Ala Glu Asn Trp Gly
115 120 125

Asp Gly Glu Pro Asn Asn Lys Lys Asn Lys Glu Asp Cys Val Glu Ile
130 135 140

Tyr Ile Lys Arg Asn Lys Asp Ala Gly Lys Trp Asn Asp Asp Ala Cys
145 150 155 160

His Lys Leu Lys Ala Ala Leu Cys Tyr Thr Ala Ser Cys Gln Pro Trp
165 170 175

Ser Cys Ser Gly His Gly Glu Cys Val Glu Ile Ile Asn Asn Tyr Thr
180 185 190

Cys Asn Cys Asp Val Gly Tyr Tyr Gly Pro Gln Cys Gln Phe Val Ile
195 200 205

Gln Cys Glu Pro Leu Glu Ala Pro Glu Leu Gly Thr Met Asp Cys Thr
210 215 220

His Ser Leu Gly Asn Phe Ser Phe Ser Ser Gln Cys Ala Phe Ser Cys
225 230 235 240

Ser Glu Gly Thr Asn Leu Thr Gly Ile Glu Glu Thr Thr Cys Gly Pro
245 250 255

Phe Gly Asn Trp Ser Ser Pro Glu Pro Thr Cys Gln Val Ile Gln Cys
260 265 270

Glu Pro Leu Ser Ala Pro Asp Leu Gly Ile Met Asn Cys Ser His Pro
275 280 285

Leu Ala Ser Phe Ser Phe Thr Ser Ala Cys Thr Phe Ile Cys Ser Glu
290 295 300

11-88L.ST25.txt

Gly Thr Glu Leu Ile Gly Lys Lys Lys Thr Ile Cys Glu Ser Ser Gly
305 310 315 320

Ile Trp Ser Asn Pro Ser Pro Ile Cys Gln Lys Leu Asp Lys Ser Phe
325 330 335

Ser Met Ile Lys Glu Gly Asp Tyr Asn Pro Leu Phe Ile Pro Val Ala
340 345 350

Val Met Val Thr Ala Phe Ser Gly Leu Ala Phe Ile Ile Trp Leu Ala
355 360 365

Arg Arg Leu Lys Lys Gly Lys Lys Ser Lys Arg Ser Met Asn Asp Pro
370 375 380

Tyr
385